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OM protein - protein search, using sw model

Run on: April 11, 2002, 10:14:10 ; Search time 266.73 Seconds  
(without alignments)  
9.369 Million cell updates/sec

Title: US-09-284-787-1  
Perfect score: 55  
Sequence: 1 YPYDVPDYA 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_AA\_Main:\*

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3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_COMB.pep.\*  
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12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep.\*  
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22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*  
23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*  
24: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	9	1 PCT-US00-05097-17	Sequence 17, Appl
2	55	100.0	9	1 PCT-US00-06950-9	Sequence 9, Appl
3	55	100.0	9	1 PCT-US00-19198-20	Sequence 20, Appl
4	55	100.0	9	1 PCT-US00-20131A-28	Sequence 28, Appl
5	55	100.0	9	1 PCT-US00-20131A-43	Sequence 43, Appl
6	55	100.0	9	1 PCT-US00-22456-1	Sequence 1, Appl
7	55	100.0	9	1 PCT-US00-23158-10	Sequence 10, Appl
8	55	100.0	9	1 PCT-US00-30238-5	Sequence 5, Appl
9	55	100.0	9	1 PCT-US93-12643-6	Sequence 6, Appl

10	55	100.0	9	1 PCT-US95-01467-14	Sequence 14, Appl
11	55	100.0	9	1 PCT-US97-15500-12	Sequence 12, Appl
12	55	100.0	9	1 PCT-US97-20344-11	Sequence 11, Appl
13	55	100.0	9	1 PCT-US97-22198-1	Sequence 1, Appl
14	55	100.0	9	1 PCT-US98-06791-1	Sequence 1, Appl
15	55	100.0	9	1 PCT-US98-11189-28	Sequence 28, Appl
16	55	100.0	9	1 PCT-US98-11189-28	Sequence 28, Appl
17	55	100.0	9	1 PCT-US99-01188-1	Sequence 1, Appl
18	55	100.0	9	1 PCT-US99-03085-93	Sequence 93, Appl
19	55	100.0	9	1 PCT-US99-04548-25	Sequence 25, Appl
20	55	100.0	9	4 US-08-017-931A-18	Sequence 18, Appl
21	55	100.0	9	4 US-08-092-977-19	Sequence 19, Appl
22	55	100.0	9	4 US-08-093-499-19	Sequence 19, Appl
23	55	100.0	9	5 US-08-108-351-7	Sequence 7, Appl
24	55	100.0	9	5 US-08-179-748-19	Sequence 19, Appl
25	55	100.0	9	5 US-08-192-477-14	Sequence 14, Appl
26	55	100.0	9	5 US-08-196-043-19	Sequence 19, Appl
27	55	100.0	9	6 US-08-287-537-3	Sequence 3, Appl
28	55	100.0	9	6 US-08-292-595-19	Sequence 19, Appl
29	55	100.0	9	6 US-08-292-595-19	Sequence 19, Appl
30	55	100.0	9	7 US-08-360-694-3	Sequence 3, Appl
31	55	100.0	9	8 US-08-443-982A-7	Sequence 7, Appl
32	55	100.0	9	8 US-08-457-263-3	Sequence 3, Appl
33	55	100.0	9	8 US-08-465-772A-28	Sequence 28, Appl
34	55	100.0	9	8 US-08-469-469A-28	Sequence 28, Appl
35	55	100.0	9	8 US-08-484-878-10	Sequence 10, Appl
36	55	100.0	9	10 US-08-619-484A-7	Sequence 7, Appl
37	55	100.0	9	10 US-08-642-120-31	Sequence 31, Appl
38	55	100.0	9	10 US-08-685-625-4	Sequence 4, Appl
39	55	100.0	9	10 US-08-690-011-17	Sequence 17, Appl
40	55	100.0	9	10 US-08-690-011-49	Sequence 49, Appl
41	55	100.0	9	11 US-08-750-111-4	Sequence 4, Appl
42	55	100.0	9	11 US-08-756-416-6	Sequence 6, Appl
43	55	100.0	9	11 US-08-793-076-54	Sequence 54, Appl
44	55	100.0	9	12 US-08-807-014-36	Sequence 36, Appl
45	55	100.0	9	24 US-60-291-149-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1  
PCT-US00-05097-17  
; Sequence 17, Application PC/TUS00005097  
; GENERAL INFORMATION:  
; APPLICANT: Washington University  
; TITLE OF INVENTION: NOVEL TRANSDUCTION MOLECULES AND METHODS  
; TITLE OF INVENTION: FOR USING SAME  
; FILE REFERENCE: 49054-PCT  
; CURRENT APPLICATION NUMBER: PCT/US00/05097  
; PRIOR FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: 60/122,757  
; PRIOR FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: 60/151,291  
; PRIOR FILING DATE: 1999-08-29  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Synthetic sequence  
PCT-US00-05097-17

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | | |  
Db 1 YPYDVPDYA 9

RESULT 2  
PCT-US00-06950-9  
; Sequence 9, Application PC/TUS0006950  
; GENERAL INFORMATION:  
; APPLICANT: VALIGENE CORPORATION  
; TITLE OF INVENTION: METHODS FOR DETECTION OF NUCLEIC ACID POLYMORPHISMS USING  
; FILE REFERENCE: 9408-042-228  
; CURRENT APPLICATION NUMBER: PCT/US00/06950  
; CURRENT FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oryctolagus cuniculus  
PCT-US00-06950-9

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 1 YPYDVPDYA 9

RESULT 3  
PCT-US00-19198-20  
; Sequence 20, Application PC/TUS0019198  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Follistatin-3  
; FILE REFERENCE: PF388PCT2  
; CURRENT APPLICATION NUMBER: PCT/US00/19198  
; CURRENT FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/144,088  
; PRIOR FILING DATE: 1999-07-16  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Primer\_Bind  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: hemagglutinin  
PCT-US00-19198-20

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 1 YPYDVPDYA 9

RESULT 4  
PCT-US00-20131A-28  
; Sequence 28, Application PC/TUS0020131A  
; GENERAL INFORMATION:  
; APPLICANT: James S. HUSTON et al.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE  
; FILE REFERENCE: INR-004PC  
; CURRENT APPLICATION NUMBER: PCT/US00/20131A

; CURRENT FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: 60/146,047  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
PCT-US00-20131A-28

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 1 YPYDVPDYA 9

RESULT 5  
PCT-US00-20131A-43  
; Sequence 43, Application PC/TUS0020131A  
; GENERAL INFORMATION:  
; APPLICANT: James S. HUSTON et al.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE  
; FILE REFERENCE: INR-004PC  
; CURRENT APPLICATION NUMBER: PCT/US00/20131A  
; CURRENT FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: 60/146,047  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
PCT-US00-20131A-43

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 1 YPYDVPDYA 9

RESULT 6  
PCT-US00-22456-1  
; Sequence 1, Application PC/TUS0022456  
; GENERAL INFORMATION:  
; APPLICANT: Donald J. Buchsbaum  
; APPLICANT: Buck E. Rogers  
; APPLICANT: Kurt R. Zinn  
; APPLICANT: David T. Curiel  
; TITLE OF INVENTION: Gene Transfer Imaging and Uses Thereof  
; FILE REFERENCE: D5836CIPPCT  
; CURRENT APPLICATION NUMBER: PCT/US00/22456  
; CURRENT FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: 09/374,972  
; PRIOR FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 6  
; SEQ ID NO 1

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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence of "HA" tag
PCT-US00-22456-1

Query Match          100.0%; Score 55; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVDPDYA 9
   | | | | | | | |
Db 1 YPYDVDPDYA 9

RESULT 7
PCT-US00-23158-10
; Sequence 10, Application PC/TUS0023158
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Sonia
; Barrios, Maria Pia
; TITLE OF INVENTION: A POLYNUCLEOTIDE ENCODING A HUMAN
; JUNCTIONAL ADHESION PROTEIN (JAM 2)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
; Suite 4700
; CITY: Chicago
; STATE: IL
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US00/23158
; FILING DATE: 23-Aug-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
PCT-US00-23158-10

Query Match          100.0%; Score 55; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVDPDYA 9
   | | | | | | | |
Db 1 YPYDVDPDYA 9

RESULT 8
PCT-US00-30238-5
; Sequence 5, Application PC/TUS0030238
; GENERAL INFORMATION:
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; APPLICANT: Lok, Si
; TITLE OF INVENTION: Cell Surface Display of Proteins by
; RECOMBINANT HOST CELLS
; FILE REFERENCE: 99-34
; CURRENT APPLICATION NUMBER: PCT/US00/30238
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hemagglutinin A epitope tag
PCT-US00-30238-5

Query Match          100.0%; Score 55; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVDPDYA 9
   | | | | | | | |
Db 1 YPYDVDPDYA 9

RESULT 9
PCT-US93-12643-6
; Sequence 6, Application PC/TUS9312643
; GENERAL INFORMATION:
; APPLICANT: Roger Brent
; APPLICANT: Antonis S. Zervos
; TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND
; RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12643
; FILING DATE: 29-DEC-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/011,398
; FILING DATE: 29-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/160001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200134
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; PCT-US93-12643-6

Query Match          100.0%; Score 55; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||

Db 1 YPYDVPDYA 9

## RESULT 10

PCT-US95-01467-14

; Sequence 14, Application PC/TUS9501467

; GENERAL INFORMATION:

; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE

; TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO

; TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Spensley Horn Juba & Lubitz

; STREET: 1880 Century Park East, Suite 500

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90067

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/01467

; FILING DATE: 03-FEB-1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bostich, June M.

; REGISTRATION NUMBER: 31,238

; REFERENCE/DOCKET NUMBER: FD-4074

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 455-5100

; TELEFAX: (619) 455-5110

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; CLONE: 12CA5

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..9

PCT-US95-01467-14

## Query Match

100.0%; Score 55; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.9e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||

Db 1 YPYDVPDYA 9

## RESULT 11

PCT-US97-15500-12

; Sequence 12, Application PC/TUS9715500

; GENERAL INFORMATION:

; APPLICANT: The General Hospital Corporation

; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/15500  
; FILING DATE: 03-SEP-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/025,370

; FILING DATE: 03-SEP-1996

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Janis K.

; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 08472/705W01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US97-15500-12

## Query Match

100.0%; Score 55; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.9e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||

Db 1 YPYDVPDYA 9

## RESULT 12

PCT-US97-20344-11

; Sequence 11, Application PC/TUS9720344

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: COMPOSITIONS AND USES FOR A NOVEL CELL

; TITLE OF INVENTION: DEATH PROTECTING PROTEIN

; NUMBER OF SEQUENCES: 12

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/20344

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US Unknown

; FILING DATE: 04-NOV-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/030,302

; FILING DATE: 05-NOV-1996

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

PCT-US97-20344-11

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
|||||

Db 1 YPYDVPDYA 9

## RESULT 13

PCT-US97-22198-1

; Sequence 1, Application PC/TUS9722198

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: INACTIVATION OF HIV CO-RECEPTORS AS THERAPY

; TITLE OF INVENTION: FOR HIV INFECTION

; NUMBER OF SEQUENCES: 6

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/22198

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/032,277

; FILING DATE: 02-DEC-1996

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

PCT-US97-22198-1

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
|||||

Db 1 YPYDVPDYA 9

## RESULT 14

PCT-US98-06791-1

; Sequence 1, Application PC/TUS9806791

; GENERAL INFORMATION:

; APPLICANT: PORT, J. D.

; APPLICANT: BRISTON, MICHAEL R.

; TITLE OF INVENTION: "TRANSGENIC MODEL AND TREATMENT FOR

; TITLE OF INVENTION: HEART DISEASE"

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SHERIDAN ROSS P.C.

; STREET: 1700 LINCOLN ST., SUITE 3500

; CITY: DENVER

; STATE: COLORADO

; COUNTRY: USA

; ZIP: 80203

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US98/06791

; FILING DATE:

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/041,966  
; FILING DATE: 03-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CROOK, WANNELL M.  
; REGISTRATION NUMBER: 31,071  
; REFERENCE/DOCKET NUMBER: 3595-2-PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 863-9700  
; TELEFAX: (303) 863-0223  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US98-06791-1

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9

|||||

Db 1 YPYDVPDYA 9

## RESULT 15

PCT-US98-11189-28

; Sequence 28, Application PC/TUS9811189

; GENERAL INFORMATION:

; APPLICANT: Nimmi, Marcel E.

; APPLICANT: Hall, Frederick L.

; APPLICANT: Wu, Lingtao

; APPLICANT: Han, Bo

; APPLICANT: Shors, Edwin

; TITLE OF INVENTION: Bone Morphogenetic

; TITLE OF INVENTION: Proteins and Their Use in Bone Growth

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merchant & Gould

; STREET: 11150 Santa Monica Boulevard, Suite 400

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90025-3395

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US98/11189

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/868,452

; FILING DATE: 3-June-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Wood, William J.

; REGISTRATION NUMBER: P-42,236

; REFERENCE/DOCKET NUMBER: 30853-1W001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 310-445-1140

; TELEFAX: 310-445-9031

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein  
PCT-US98-111189-28

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
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Db 1 YPYDVPDYA 9

Search completed: April 11, 2002, 10:20:50  
Job time: 400 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2002, 10:14:10 ; Search time 39.37 Seconds  
(without alignments)  
16.824 Million cell updates/sec

Title: US-09-284-787-1  
Perfect score: 55  
Sequence: 1 YPVDVPOYA 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 367557 seqs, 73597022 residues

Total number of hits satisfying chosen parameters: 367557

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*  
1: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.1\*  
7: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*  
8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9	1	PCT-US01-45076-9
2	55	100.0	9	5	US-09-466-568-19
3	55	100.0	9	5	US-09-931-381A-24
4	55	100.0	9	5	US-09-936-969-9
5	55	100.0	9	5	US-09-180-167A-17
6	55	100.0	9	5	US-09-775-052A-17
7	55	100.0	9	6	US-09-912-733-32
8	55	100.0	9	6	US-09-574-735C-45
9	55	100.0	9	6	US-09-852-370A-33
10	55	100.0	9	6	US-09-906-393A-4
11	55	100.0	9	6	US-09-775-052-17
12	55	100.0	9	6	US-09-554-726A-53
13	55	100.0	9	6	US-09-845-667-32
14	55	100.0	9	6	US-09-995-847-4
15	55	100.0	9	6	US-09-554-726A-53
16	55	100.0	9	6	US-09-529-106A-16
17	55	100.0	9	6	US-09-713-858-7
18	55	100.0	9	6	US-09-714-471-7
19	55	100.0	9	6	US-09-896-515-37
20	55	100.0	9	6	US-09-598-347-7
21	55	100.0	9	6	US-09-830-980-8
22	55	100.0	9	6	US-09-848-813-5
23	55	100.0	9	6	US-09-918-036-17
24	55	100.0	9	6	US-09-922-226-40
25	55	100.0	9	6	US-09-807-305A-3

26	55	100.0	9	6	US-09-352-171-7	Sequence 7, Appl
27	55	100.0	9	6	US-09-620-955B-28	Sequence 28, Appl
28	55	100.0	9	6	US-09-620-955B-43	Sequence 43, Appl
29	55	100.0	9	7	US-10-001-073-23	Sequence 23, Appl
30	55	100.0	9	7	US-10-066-151-93	Sequence 93, Appl
31	55	100.0	9	7	US-10-003-496-16	Sequence 16, Appl
32	55	100.0	9	7	US-10-009-178-10	Sequence 10, Appl
33	55	100.0	9	7	US-10-083-815-7	Sequence 7, Appl
34	55	100.0	9	7	US-10-059-720-49	Sequence 49, Appl
35	55	100.0	9	7	US-10-084-706-55	Sequence 55, Appl
36	55	100.0	10	5	US-09-563-055A-1	Sequence 1, Appl
37	55	100.0	10	6	US-09-453-234-30	Sequence 30, Appl
38	55	100.0	10	6	US-09-589-619-10	Sequence 10, Appl
39	55	100.0	10	6	US-09-563-055-1	Sequence 1, Appl
40	55	100.0	10	6	US-09-994-487-1	Sequence 1, Appl
41	55	100.0	10	6	US-09-645-456-25	Sequence 25, Appl
42	55	100.0	10	6	US-09-900-590A-28	Sequence 28, Appl
43	55	100.0	10	6	US-09-822-295-13	Sequence 13, Appl
44	55	100.0	11	5	US-09-415-765A-2	Sequence 2, Appl
45	55	100.0	11	5	US-09-626-580B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
PCT-US01-45076-9  
; Sequence 9, Application PC/TUS0145076  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation  
; APPLICANT: Scadden, David T.  
; APPLICANT: Lee, Byeong-Chel  
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR MANIPULATING  
; TITLE OF INVENTION: HEMATOPOIETIC STEM CELLS  
; FILE REFERENCE: M0765/7039MO/ERG/KA  
; CURRENT APPLICATION NUMBER: PCT/US01/45076  
; CURRENT FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: U.S. 60/250,727  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HA-tag  
PCT-US01-45076-9

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPVDVPOYA 9  
| | | | | | | | | |  
Db 1 YPVDVPOYA 9

RESULT 2  
US-09-466-568-19  
; Sequence 19, Application US/09466568  
; GENERAL INFORMATION:  
; APPLICANT: Crabtree, Gerald R.  
; APPLICANT: Schreiber, Stuart L.  
; APPLICANT: Spencer, David M.  
; APPLICANT: Wandless, Thomas J.  
; APPLICANT: Beishaw, Peter  
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED  
; GENES AND OTHER BIOLOGICAL EVENTS  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.

STREET: 26 Landsdowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC/DOS/MS/DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/466,568  
FILING DATE: 17-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/157,753  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/388,653  
FILING DATE: 14-FEB-1995  
APPLICATION NUMBER: US 08/478,386  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Figg, E. Anthony  
REGISTRATION NUMBER: 27,195  
REFERENCE/DOCKET NUMBER: 2054-114A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-466-568-19

Query Match 100.0%; Score 55; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | |  
DB 1 YPYDVPDYA 9

RESULT 3  
US-09-931-381A-24  
; Sequence 24, Application US/09931381A  
; GENERAL INFORMATION:  
; APPLICANT: Butcher, Eugene C.  
; APPLICANT: Kunkel, Eric J.  
; APPLICANT: Pan, Junliang  
; APPLICANT: Soler-Ferran, Dulce  
; TITLE OF INVENTION: Method for Identifying Agents Which  
; TITLE OF INVENTION: Modulate Chemokine "Mec"-Induced Functions of CCR3 and/or  
; TITLE OF INVENTION: CCR10  
; FILE REFERENCE: 1855.2010-003  
; CURRENT APPLICATION NUMBER: US/09/931,381A  
; CURRENT FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: U.S. 09/638,914  
; PRIOR FILING DATE: 2000-08-15  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Influenza virus  
US-09-931-381A-24

Query Match 100.0%; Score 55; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YPYDVPDYA 9  
| | | | | | | | |  
DB 1 YPYDVPDYA 9  
RESULT 4  
US-09-936-969-9  
; Sequence 9, Application US/09936969  
; GENERAL INFORMATION:  
; APPLICANT: Iris, F.  
; APPLICANT: Pourny, J.  
; TITLE OF INVENTION: METHODS FOR DETECTION OF NUCLEIC ACID POLYMORPHISMS USING  
; TITLE OF INVENTION: PEPTIDE-LABELED OLIGONUCLEOTIDES AND ANTIBODY ARRAYS  
; FILE REFERENCE: 9408-042-999  
; CURRENT APPLICATION NUMBER: US/09/936,969  
; CURRENT FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oryctolagus cuniculus  
US-09-936-969-9

Query Match 100.0%; Score 55; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | |  
DB 1 YPYDVPDYA 9

RESULT 5  
US-09-180-167A-17  
; Sequence 17, Application US/09180167A  
; GENERAL INFORMATION:  
; APPLICANT: Gordon C. Shore et al.  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING  
; TITLE OF INVENTION: APOPTOSIS  
; FILE REFERENCE: 50013/004003  
; CURRENT APPLICATION NUMBER: US/09/180,167A  
; CURRENT FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: CA 2,198,988  
; PRIOR FILING DATE: 1997-03-03  
; PRIOR APPLICATION NUMBER: PCT/IB98/00706  
; PRIOR FILING DATE: 1998-03-02  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic, based on Orthomyxoviridae Influenza A  
; OTHER INFORMATION: virus  
US-09-180-167A-17

Query Match 100.0%; Score 55; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | |  
DB 1 YPYDVPDYA 9



RESULT 6  
US-09-775-052A-17  
; Sequence 17, Application US/09775052A  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 4888J/1742  
; CURRENT APPLICATION NUMBER: US/09/775.052A  
; CURRENT FILING DATE: 2001-12-05  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208.966  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069.012  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052A-17

Query Match 100.0%; Score 55; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | |  
Db 1 YPYDVPDYA 9

RESULT 7  
US-09-912-733-32  
; Sequence 32, Application US/09912733  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Michael  
; TITLE OF INVENTION: DNA SEQUENCES, VECTORS, AND FUSION POLYPEPTIDES FOR SECRETION OF  
; FILE REFERENCE: A-62926-1  
; CURRENT APPLICATION NUMBER: US/09/912.733  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR FILING DATE: 1997-01-17  
; PRIOR APPLICATION NUMBER: US 08/785,668  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic.  
US-09-912-733-32

Query Match 100.0%; Score 55; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | |  
Db 1 YPYDVPDYA 9

RESULT 8  
US-09-574-735C-45  
; Sequence 45, Application US/09574735C  
; GENERAL INFORMATION:  
; APPLICANT: De Veylder, Lieven  
; APPLICANT: Beeckman, Tom  
; APPLICANT: Inz, Dirk  
; APPLICANT: Van Camp, Wim

Query Match 100.0%; Score 55; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | |  
Db 1 YPYDVPDYA 9

RESULT 9  
US-09-574-735C-45  
; Sequence 45, Application US/09574735C  
; GENERAL INFORMATION:  
; APPLICANT: Pomerantz, Joel L.  
; APPLICANT: Sharp, Phillip A.  
; APPLICANT: Babot, Carl O.  
; TITLE OF INVENTION: Chimeric DNA-binding proteins  
; FILE REFERENCE: APV-022.02  
; CURRENT APPLICATION NUMBER: US/09/574.735C  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: PCT/US95/16982  
; PRIOR FILING DATE: 1995-12-29  
; PRIOR APPLICATION NUMBER: 08/366,083  
; PRIOR FILING DATE: 1994-12-29  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 33  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: encoded  
; OTHER INFORMATION: epitope  
US-09-574-735C-45

Query Match 100.0%; Score 55; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | |  
Db 1 YPYDVPDYA 9

RESULT 10  
US-09-906-393A-4  
; Sequence 4, Application US/09906393A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Zhou  
; APPLICANT: Xiao, Wuhan  
; TITLE OF INVENTION: METHOD OF PROGNOSTICATING CANCER AND THE PROTEINS INVOLVED  
; FILE REFERENCE: 1720-1-001CIP  
; CURRENT APPLICATION NUMBER: US/09/906.393A  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/218,761  
; PRIOR FILING DATE: 2000-07-17

Query Match 100.0%; Score 55; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | |  
Db 1 YPYDVPDYA 9

; APPLICANT: Ktols, Luc  
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof  
; FILE REFERENCE: 2283/301  
; CURRENT APPLICATION NUMBER: US/09/574.735C  
; CURRENT FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 45  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: HA-epitope  
US-09-574-735C-45

Query Match 100.0%; Score 55; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | |  
Db 1 YPYDVPDYA 9

RESULT 9  
US-09-852-370A-33  
; Sequence 33, Application US/09852370A  
; GENERAL INFORMATION:  
; APPLICANT: Pomerantz, Joel L.  
; APPLICANT: Sharp, Phillip A.  
; APPLICANT: Babot, Carl O.  
; TITLE OF INVENTION: Chimeric DNA-binding proteins  
; FILE REFERENCE: APV-022.02  
; CURRENT APPLICATION NUMBER: US/09/852.370A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: PCT/US95/16982  
; PRIOR FILING DATE: 1995-12-29  
; PRIOR APPLICATION NUMBER: 08/366,083  
; PRIOR FILING DATE: 1994-12-29  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 33  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: encoded  
; OTHER INFORMATION: epitope  
US-09-852-370A-33

Query Match 100.0%; Score 55; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | |  
Db 1 YPYDVPDYA 9

RESULT 10  
US-09-906-393A-4  
; Sequence 4, Application US/09906393A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Zhou  
; APPLICANT: Xiao, Wuhan  
; TITLE OF INVENTION: METHOD OF PROGNOSTICATING CANCER AND THE PROTEINS INVOLVED  
; FILE REFERENCE: 1720-1-001CIP  
; CURRENT APPLICATION NUMBER: US/09/906.393A  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/218,761  
; PRIOR FILING DATE: 2000-07-17

Query Match 100.0%; Score 55; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | |  
Db 1 YPYDVPDYA 9

; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: HA Tag  
US-09-906-393A-4

Query Match 100.0%; Score 55; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 1 YPYDVPDYA 9

RESULT 11  
US-09-775-052-17  
; Sequence 17, Application US/09775052  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 09/208,966  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/082,402  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052-17

Query Match 100.0%; Score 55; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 1 YPYDVPDYA 9

RESULT 12  
US-09-554-726A-53  
; Sequence 53, Application US/09554726A  
; GENERAL INFORMATION:  
; APPLICANT: HERMANN, Bernhard  
; APPLICANT: KOSCHORZ, Birgit  
; APPLICANT: KISPERT, Andreas  
; TITLE OF INVENTION: NUCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATION THEREOF  
; FILE REFERENCE: 258.0009 0101  
; CURRENT APPLICATION NUMBER: US/09/554, 726A  
; CURRENT FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: PCT/EP 98/07395  
; PRIOR FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: EP 98 10 3596.7  
; PRIOR FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: EP 97 12 0190.0  
; PRIOR FILING DATE: 1997-11-18  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 53  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide  
US-09-554-726A-53

Query Match 100.0%; Score 55; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 1 YPYDVPDYA 9

RESULT 13  
US-09-845-667-32  
; Sequence 32, Application US/09845667  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Philip  
; APPLICANT: Alessi, Dario  
; APPLICANT: Cross, Darren  
; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD FOR AGENTS  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Braman & Rogalskyj, LLP  
; STREET: P.O. Box 352  
; CITY: Canandaigua  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 14424-0352  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/845,667  
; FILING DATE: 30-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/091,763  
; FILING DATE: 19-JUN-1998  
; APPLICATION NUMBER: PCT/GB96/03186  
; FILING DATE: 20-DEC-1996  
; APPLICATION NUMBER: GB 9526083.2  
; FILING DATE: 20-DEC-1995  
; APPLICATION NUMBER: GB 9610272.8  
; FILING DATE: 16-MAY-1996  
; APPLICATION NUMBER: GB 9615066.9  
; FILING DATE: 18-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Braman, Susan J  
; REGISTRATION NUMBER: 34,103  
; REFERENCE/DOCKET NUMBER: 002.00041  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 716-393-3002  
; TELEFAX: 716-393-3001  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-845-667-32

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Query Match      100.0%; Score 55; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9
   |||||
Db 1 YPYDVPDYA 9

RESULT 14
US-09-995-847-4
; Sequence 4, Application US/09995847
; GENERAL INFORMATION:
; APPLICANT: Rizzuto, Carlo
; APPLICANT: Afeyan, Noubar
; APPLICANT: Lee, Frank
; APPLICANT: Church, George
; APPLICANT: Das Gupta, Ruchira
; APPLICANT: Zhang, Bin
; APPLICANT: Schwartz, John
; APPLICANT: Lugovskoy, Alexey
; TITLE OF INVENTION: MODULAR MOLECULAR CLASPS AND USES THEREOF
; FILE REFERENCE: ENZ-001
; CURRENT APPLICATION NUMBER: US/09/995,847
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/279,524
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HA epitope
US-09-995-847-4
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Search completed: April 11, 2002, 10:21:36  
Job time: 446 sec

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US-09-554-726A-53

Query Match      100.0%; Score 55; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9
   |||||
Db 1 YPYDVPDYA 9
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Query Match      100.0%; Score 55; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9
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Db 1 YPYDVPDYA 9
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RESULT 15
US-09-554-726A-53
; Sequence 53, Application US/09554726A
; GENERAL INFORMATION:
; APPLICANT: HERRMANN, Bernhard
; APPLICANT: KOSCHORZ, Birgit
; APPLICANT: KISPERT, Andreas
; TITLE OF INVENTION: NUCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATION THEREOF
; FILE REFERENCE: 258.0009 0101
; CURRENT APPLICATION NUMBER: US/09/554,726A
; CURRENT FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: PCT/EP 98/07395
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: EP 98 10 3596.7
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: EP 97 12 0190.0
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2002, 10:20:50 ; Search time 266.73 Seconds  
(without alignments)  
14.574 Million cell updates/sec

Title: US-09-284-787-2  
Perfect score: 80  
Sequence: 1 YPYDVPDYAGSGSK 14

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

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24: /cgn2\_6/ptodata/2/paa/us60\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	80	100.0	14	16 US-09-284-787-2	Sequence 2, Appli
2	75	93.8	165	21 US-09-780-224A-11	Sequence 11, Appl
3	68	85.0	32	18 US-09-475-158-56	Sequence 56, Appl
4	67	83.8	126	20 US-09-622-646-23	Sequence 23, Appl
5	67	83.8	143	20 US-09-622-646-22	Sequence 22, Appl
6	67	83.8	147	20 US-09-622-646-25	Sequence 25, Appl
7	65	81.2	16	1 PCT-US00-09002-11	Sequence 11, Appl
8	65	81.2	16	1 PCT-US98-16887-7	Sequence 7, Appli
9	65	81.2	16	15 US-09-134-793-7	Sequence 7, Appli

10	65	81.2	16	15 US-09-134-793A-7	Sequence 7, Appli
11	65	81.2	16	17 US-09-300-639B-4	Sequence 4, Appli
12	65	81.2	16	18 US-09-459-113A-15	Sequence 15, Appl
13	65	81.2	16	19 US-09-514-673-15	Sequence 51, Appl
14	65	81.2	17	11 US-08-787-738-51	Sequence 51, Appl
15	65	81.2	17	11 US-08-787-738B-51	Sequence 51, Appl
16	65	81.2	17	13 US-08-963-368-51	Sequence 51, Appl
17	65	81.2	25	10 US-08-642-120-27	Sequence 27, Appl
18	65	81.2	28	5 US-08-108-351-4	Sequence 4, Appli
19	65	81.2	346	16 US-09-215-569B-8	Sequence 8, Appli
20	63	78.8	15	13 US-08-935-088-5	Sequence 5, Appli
21	62	77.5	219	16 US-09-201-931-2	Sequence 2, Appli
22	62	77.5	219	22 US-09-847-185-2	Sequence 2, Appli
23	61	76.2	10	19 US-09-546-238-13	Sequence 13, Appl
24	61	76.2	10	23 US-09-954-043-13	Sequence 13, Appl
25	61	76.2	12	14 US-09-023-905-16	Sequence 16, Appl
26	61	76.2	21	7 US-08-361-811-127	Sequence 127, App
27	61	76.2	21	7 US-08-381-478-169	Sequence 169, App
28	61	76.2	21	9 US-08-535-025-169	Sequence 169, App
29	61	76.2	21	9 US-08-591-919-169	Sequence 169, App
30	61	76.2	21	9 US-08-592-007-169	Sequence 169, App
31	61	76.2	21	9 US-08-592-027-169	Sequence 169, App
32	61	76.2	21	9 US-08-592-131-169	Sequence 169, App
33	61	76.2	21	13 US-08-964-039-169	Sequence 169, App
34	61	76.2	45	23 US-09-921-144-6	Sequence 6, Appli
35	61	76.2	48	23 US-09-921-144-8	Sequence 8, Appli
36	61	76.2	67	23 US-09-921-144-10	Sequence 10, Appl
37	61	76.2	70	23 US-09-921-144-12	Sequence 12, Appl
38	61	76.2	162	23 US-09-921-144-16	Sequence 16, Appl
39	61	76.2	163	23 US-09-921-144-14	Sequence 14, Appl
40	61	76.2	184	23 US-09-921-144-20	Sequence 20, Appl
41	61	76.2	185	23 US-09-921-144-18	Sequence 18, Appl
42	61	76.2	371	22 US-09-849-243-16	Sequence 16, Appl
43	60.5	75.6	102	8 US-08-467-551-2	Sequence 2, Appli
44	60.5	75.6	272	8 US-08-467-551-6	Sequence 6, Appli
45	60	75.0	272	8 US-08-478-408-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-284-787-2  
; Sequence 2, Application US/09284787  
; GENERAL INFORMATION:  
; APPLICANT: Roche Diagnostics GmbH  
; TITLE OF INVENTION: Monoclonal Antibodies Against the Epitope YPYDVPDYA, A Process  
; TITLE OF INVENTION: Producing the Same and their Use  
; FILE REFERENCE: BMID9913US  
; CURRENT APPLICATION NUMBER: US/09/284,787  
; PRIOR FILING DATE: 1999-08-16  
; PRIOR FILING DATE: 1997-10-20  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 2  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: human influenza virus  
US-09-284-787-2

Query Match 100.0%; Score 80; DB 16; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.1e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGSGSK 14  
| | | | | | | | | | | | | | | |  
Db 1 YPYDVPDYAGSGSK 14

RESULT 2  
US-09-780-224A-11

```
; Sequence 11, Application US/09780224A
; GENERAL INFORMATION:
; APPLICANT: Roelvink, Petrus W
; APPLICANT: Kovessdi, Imre
; APPLICANT: Wickham, Thomas J
; TITLE OF INVENTION: ADENOVIRAL CAPSID CONTAINING CHIMERIC PROTEIN IX
; FILE REFERENCE: 208859
; CURRENT APPLICATION NUMBER: US/09/780,224A
; CURRENT FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-780-224A-11

Query Match      93.8%; Score 75; DB 21; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPDVDPYAGSGS 13
Db 4 YPDVDPYAGSGS 16

RESULT 3
US-09-475-158-56
; Sequence 56, Application US/09475158
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: PTH Functional Domain Conjugate Peptides, Derivatives
; TITLE OF INVENTION: Thereof and Novel Tethered Ligand-Receptor Molecules
; FILE REFERENCE: 0609,4780001
; CURRENT APPLICATION NUMBER: US/09/475,158
; CURRENT FILING DATE: 1999-12-30
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified PTH
US-09-475-158-56

Query Match      85.0%; Score 68; DB 18; Length 32;
Best Local Similarity 78.6%; Pred. No. 0.001;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YPDVDPYAGSGSK 14
Db 10 YPDVDPYAGGGGE 23

RESULT 4
US-09-622-646-23
; Sequence 23, Application US/09622646
; GENERAL INFORMATION:
; APPLICANT: OZAKI, YASUO
; APPLICANT: KOISHIHARA, YASUO
; TITLE OF INVENTION: IMMUNOCHEMICAL ASSAY FOR ANTI-HM1.24 ANTIBODY
; FILE REFERENCE: 053466/0286

Query Match      83.8%; Score 67; DB 20; Length 143;
Best Local Similarity 78.6%; Pred. No. 0.0084;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YPDVDPYAGSGSK 14
Db 1 YPDVDPYAGTNS 14

RESULT 5
US-09-622-646-22
; Sequence 22, Application US/09622646
; GENERAL INFORMATION:
; APPLICANT: OZAKI, YASUO
; APPLICANT: KOISHIHARA, YASUO
; TITLE OF INVENTION: IMMUNOCHEMICAL ASSAY FOR ANTI-HM1.24 ANTIBODY
; FILE REFERENCE: 053466/0286
; CURRENT APPLICATION NUMBER: US/09/622,646
; CURRENT FILING DATE: 2001-05-30
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/Jp99/00885
; PRIOR FILING DATE: 1999-02-25
; PRIOR FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of a fusion protein comprising HA peptide and soluble
; OTHER INFORMATION: HM 1.24 antigenic protein
US-09-622-646-22

Query Match      83.8%; Score 67; DB 20; Length 126;
Best Local Similarity 78.6%; Pred. No. 0.0073;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YPDVDPYAGSGSK 14
Db 1 YPDVDPYAGTNS 14

RESULT 6
US-09-622-646-25
; Sequence 25, Application US/09622646
; GENERAL INFORMATION:
; APPLICANT: OZAKI, YASUO
; APPLICANT: KOISHIHARA, YASUO
; TITLE OF INVENTION: IMMUNOCHEMICAL ASSAY FOR ANTI-HM1.24 ANTIBODY
; FILE REFERENCE: 053466/0286
; CURRENT APPLICATION NUMBER: US/09/622,646
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; CURRENT APPLICATION NUMBER: US/09/622,646
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/Jp99/00885
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: JP 10-60613
; PRIOR FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of a fusion protein comprising HA peptide and
; OTHER INFORMATION: C-terminal-lacking soluble HM 1.24 antigenic protein
US-09-622-646-23
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Query Match      83.8%; Score 67; DB 20; Length 126;
Best Local Similarity 78.6%; Pred. No. 0.0073;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 YPDVDPYAGSGSK 14
Db 1 YPDVDPYAGTNS 14
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## RESULT 5

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US-09-622-646-22
; Sequence 22, Application US/09622646
; GENERAL INFORMATION:
; APPLICANT: OZAKI, YASUO
; APPLICANT: KOISHIHARA, YASUO
; TITLE OF INVENTION: IMMUNOCHEMICAL ASSAY FOR ANTI-HM1.24 ANTIBODY
; FILE REFERENCE: 053466/0286
; CURRENT APPLICATION NUMBER: US/09/622,646
; CURRENT FILING DATE: 2001-05-30
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/Jp99/00885
; PRIOR FILING DATE: 1999-02-25
; PRIOR FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of a fusion protein comprising HA peptide and soluble
; OTHER INFORMATION: HM 1.24 antigenic protein
US-09-622-646-22
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Query Match      83.8%; Score 67; DB 20; Length 143;
Best Local Similarity 78.6%; Pred. No. 0.0084;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 YPDVDPYAGSGSK 14
Db 1 YPDVDPYAGTNS 14
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## RESULT 6

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US-09-622-646-25
; Sequence 25, Application US/09622646
; GENERAL INFORMATION:
; APPLICANT: OZAKI, YASUO
; APPLICANT: KOISHIHARA, YASUO
; TITLE OF INVENTION: IMMUNOCHEMICAL ASSAY FOR ANTI-HM1.24 ANTIBODY
; FILE REFERENCE: 053466/0286
; CURRENT APPLICATION NUMBER: US/09/622,646
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; CURRENT FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/JP99/00885  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: JP 10-60613  
; PRIOR FILING DATE: 1998-02-25  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 147  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence  
; OTHER INFORMATION: of CG M/HA-HM164  
; US-09-622-646-25

Query Match 83.8%; Score 67; DB 20; Length 147;  
Best Local Similarity 78.6%; Pred. No. 0.0087;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSGSK 14  
Db 22 YPYDVPDYAGTNS 35

RESULT 7  
PCT-US00-09002-11  
; Sequence 11, Application PC/TUS0009002  
; GENERAL INFORMATION:  
; APPLICANT: Mayo Foundation for Medical Education and Research et al.  
; TITLE OF INVENTION: Anti-apoptotic fusion polypeptide  
; FILE REFERENCE: 130.195W01  
; CURRENT APPLICATION NUMBER: PCT/US00/09002  
; CURRENT FILING DATE: 2000-04-07  
; EARLIER APPLICATION NUMBER: US 60/128,021  
; EARLIER FILING DATE: 1999-04-06  
; EARLIER APPLICATION NUMBER: US 60/127,867  
; EARLIER FILING DATE: 1999-04-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PTAT-HA linker  
PCT-US00-09002-11

Query Match 81.2%; Score 65; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGS 11  
Db 4 YPYDVPDYAGS 14

RESULT 8  
PCT-US98-16887-7  
; Sequence 7, Application PC/TUS9816887  
; GENERAL INFORMATION:  
; APPLICANT: Washington University  
; TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA

; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/16887  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/056,713  
; FILING DATE: 22-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 47275-PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US98-16887-7

Query Match 81.2%; Score 65; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGS 11  
Db 4 YPYDVPDYAGS 14

RESULT 9  
US-09-134-793-7  
; Sequence 7, Application US/09134793  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; APPLICANT: Jesse, Joel A.  
; TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM  
; TITLE OF INVENTION: AND USE THEREOF  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/134,793  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/056,713  
; FILING DATE: 22-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 47275  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-134-793-7

Query Match 81.2%; Score 65; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGS 11  
| | | | | | | | | |  
Db 4 YPYDVPDYAGS 14

RESULT 10  
US-09-134-793A-7

; Sequence 7, Application US/09134793A  
; GENERAL INFORMATION:  
; APPLICANT: DOMDY, STEVEN F.  
; APPLICANT: JESSEE, JOEL A.  
; TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM AND USE THEREOF  
; FILE REFERENCE: 1742/47275  
; CURRENT APPLICATION NUMBER: US/09/134,793A  
; CURRENT FILING DATE: 1998-08-14  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: pTAT-HA linker  
US-09-134-793A-7

Query Match 81.2%; Score 65; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGS 11  
| | | | | | | | | |  
Db 4 YPYDVPDYAGS 14

RESULT 11  
US-09-300-639B-4

; Sequence 4, Application US/09300639B  
; GENERAL INFORMATION:  
; APPLICANT: Steven F. Dowdy  
; TITLE OF INVENTION: Methods for Transducing Fusion Molecules  
; FILE REFERENCE: 48031  
; CURRENT APPLICATION NUMBER: US/09/300,639B  
; CURRENT FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/083,380  
; PRIOR FILING DATE: 1998-04-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of pTAT-HA plasmid linker sequence  
US-09-300-639B-4

Query Match 81.2%; Score 65; DB 17; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGS 11  
| | | | | | | | | |  
Db 4 YPYDVPDYAGS 14

RESULT 12

US-09-459-113A-15  
; Sequence 15, Application US/09459113A  
; GENERAL INFORMATION:  
; APPLICANT: Steven F. Dowdy  
; TITLE OF INVENTION: PROTEIN TRANSDUCTION SYSTEM AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 48,884 (1742)  
; CURRENT APPLICATION NUMBER: US/09/459,113A  
; CURRENT FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: 60/111,701  
; PRIOR FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Synthetic pTAT-HA linker  
US-09-459-113A-15

Query Match 81.2%; Score 65; DB 18; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGS 11  
| | | | | | | | | |  
Db 4 YPYDVPDYAGS 14

RESULT 13

US-09-514-673-15  
; Sequence 15, Application US/09514673  
; GENERAL INFORMATION:  
; APPLICANT: DOMDY, STEVEN F.  
; TITLE OF INVENTION: NOVEL TRANSDUCTION MOLECULES AND METHODS FOR USING SAME  
; FILE REFERENCE: 49054(71742)  
; CURRENT APPLICATION NUMBER: US/09/514,673  
; CURRENT FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/122,757  
; PRIOR FILING DATE: 1999-02-28  
; PRIOR APPLICATION NUMBER: 60/151,291  
; PRIOR FILING DATE: 1999-08-29  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: pTAT-HA linker  
US-09-514-673-15

Query Match 81.2%; Score 65; DB 19; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGS 11  
| | | | | | | | | |  
Db 4 YPYDVPDYAGS 14



Qy 1 YPYDVDPYAGS 11  
|||  
pb 5 YPYDVDPYAGS 15

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OM protein - protein search, using sw model

Run on: April 11, 2002, 10:21:36 ; Search time 39.37 Seconds  
(without alignments)  
26.171 Million cell updates/sec

Title: US-09-284-787-2

Perfect score: 80

Sequence: 1 YPYDVPDYAGSGSK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 367557 seqs, 73597022 residues

Total number of hits satisfying chosen parameters: 367557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA.New.\*

1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.1\*  
7: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*  
8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	88.8	34	6	US-09-896-915-8
2	65	81.2	16	5	US-09-775-052A-15
3	65	81.2	16	6	US-09-775-052-15
4	65	81.2	17	6	US-09-916-940-51
5	65	81.2	17	7	US-10-096-550-51
6	63	78.8	86	5	US-09-892-208A-2
7	63	78.8	86	7	US-10-028-247-2
8	59	73.8	14	6	US-09-740-876-1
9	59	73.8	19	5	US-09-415-765A-57
10	59	73.8	19	5	US-09-626-580B-57
11	59	73.8	19	5	US-09-626-581C-57
12	59	73.8	26	6	US-09-481-620A-34
13	59	73.8	27	6	US-09-620-955B-31
14	59	73.8	27	7	US-10-002-244-33
15	59	73.8	41	6	US-09-481-620A-24
16	59	73.8	41	7	US-10-002-244-25
17	59	73.8	389	5	US-09-832-161-14
18	58.5	73.1	540	7	US-10-015-535-22
19	58.5	73.1	540	7	US-10-015-535-30
20	57	71.2	13	5	US-09-395-061-4
21	55	68.8	9	1	PCT-US01-45076-9
22	55	68.8	9	5	US-09-466-568-19
23	55	68.8	9	5	US-09-931-381A-24
24	55	68.8	9	5	US-09-936-969-9
25	55	68.8	9	5	US-09-180-167A-17
26	55	68.8	9	5	US-09-180-167A-17

26 55 68.8 9 5 US-09-775-052A-17 Sequence 17, Appl  
27 55 68.8 9 6 US-09-912-733-32 Sequence 32, Appl  
28 55 68.8 9 6 US-09-574-735C-45 Sequence 45, Appl  
29 55 68.8 9 6 US-09-852-370A-33 Sequence 33, Appl  
30 55 68.8 9 6 US-09-906-393A-4 Sequence 4, Appl  
31 55 68.8 9 6 US-09-775-052-17 Sequence 17, Appl  
32 55 68.8 9 6 US-09-554-726A-53 Sequence 53, Appl  
33 55 68.8 9 6 US-09-845-667-32 Sequence 32, Appl  
34 55 68.8 9 6 US-09-995-847-4 Sequence 4, Appl  
35 55 68.8 9 6 US-09-554-726A-53 Sequence 53, Appl  
36 55 68.8 9 6 US-09-529-106A-16 Sequence 16, Appl  
37 55 68.8 9 6 US-09-713-858-7 Sequence 7, Appl  
38 55 68.8 9 6 US-09-714-471-7 Sequence 7, Appl  
39 55 68.8 9 6 US-09-896-915-37 Sequence 37, Appl  
40 55 68.8 9 6 US-09-598-347-7 Sequence 7, Appl  
41 55 68.8 9 6 US-09-830-980-8 Sequence 8, Appl  
42 55 68.8 9 6 US-09-848-813-5 Sequence 5, Appl  
43 55 68.8 9 6 US-09-918-036-17 Sequence 17, Appl  
44 55 68.8 9 6 US-09-922-226-40 Sequence 40, Appl  
45 55 68.8 9 6 US-09-807-305A-3 Sequence 3, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-896-915-8  
; Sequence 8, Application US/09896915  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; APPLICANT: Griffiths, Andrew  
; TITLE OF INVENTION: Optical Sorting Method  
; FILE REFERENCE: 18396/2022  
; CURRENT APPLICATION NUMBER: US/09/896,915  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: GB9900298.2  
; PRIOR FILING DATE: 1999-01-07  
; PRIOR APPLICATION NUMBER: PCT/GB00/00030  
; PRIOR FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: plasmid pET-23d(FLAGHA)  
US-09-896-915-8

Query Match 88.8%; Score 71; DB 6; Length 34;  
Best Local Similarity 92.3%; Pred. NO. 3.7e-05;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

##### QY 1 YPYDVPDYAGSGS 13

|||||||

##### Db 22 YPYDVPDYAGSGS 34

##### RESULT 2

US-09-775-052A-15  
; Sequence 15, Application US/09775052A  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052A  
; CURRENT FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15

; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052A-15

Query Match 81.2%; Score 65; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGS 11  
| | | | | | | | | | | |  
Db 4 YPYDVPDYAGS 14

RESULT 3  
US-09-775-052-15  
; Sequence 15, Application US/09775052  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 09/208,966  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/082,402  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052-15

Query Match 81.2%; Score 65; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGS 11  
| | | | | | | | | | | |  
Db 4 YPYDVPDYAGS 14

RESULT 4  
US-09-916-940-51  
; Sequence 51, Application US/09916940  
; GENERAL INFORMATION:  
; APPLICANT: Nolan, Garry P  
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR  
; FILE REFERENCE: A-64260-6/RMS/AMS  
; CURRENT APPLICATION NUMBER: US/09/916,940  
; CURRENT FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: US 09/727,715  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 08/963,368  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: US 08/589,109  
; PRIOR FILING DATE: 1996-01-23  
; PRIOR APPLICATION NUMBER: US 08/589,911  
; PRIOR FILING DATE: 1996-01-23  
; PRIOR APPLICATION NUMBER: US 08/789,333  
; PRIOR FILING DATE: 1997-01-23  
; PRIOR APPLICATION NUMBER: US 08/787,738  
; PRIOR FILING DATE: 1997-01-23  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51

; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: epitope tag  
; OTHER INFORMATION: sequence.  
US-09-916-940-51

Query Match 81.2%; Score 65; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGS 11  
| | | | | | | | | | | |  
Db 5 YPYDVPDYAGS 15

RESULT 5  
US-10-096-550-51  
; Sequence 51, Application US/10096550  
; GENERAL INFORMATION:  
; APPLICANT: Nolan, Garry P  
; APPLICANT: Rothenburg, Michael S.  
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR  
; FILE REFERENCE: A-64259-1 correction  
; CURRENT APPLICATION NUMBER: US/10/096,550  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 08/787,738  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: 08/589,108  
; PRIOR FILING DATE: 1996-01-23  
; PRIOR APPLICATION NUMBER: 08/589,911  
; PRIOR FILING DATE: 1996-01-23  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.  
US-10-096-550-51

Query Match 81.2%; Score 65; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGS 11  
| | | | | | | | | | | |  
Db 5 YPYDVPDYAGS 15

RESULT 6  
US-09-892-208A-2  
; Sequence 2, Application US/09892208A  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Stanley  
; APPLICANT: Lathrop, Stephanie J.  
; APPLICANT: Longchamp, Pascal F.  
; APPLICANT: Whalen, Robert G.  
; APPLICANT: Maxygen, Inc.  
; TITLE OF INVENTION: Methods and Compositions for Developing Spore Display  
; FILE REFERENCE: 18097A-03351005  
; CURRENT APPLICATION NUMBER: US/09/892,208A  
; CURRENT FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: US 60/214,161  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
; FEATURE:  
; OTHER INFORMATION: CotC27 including HALL epitope region  
US-09-892-208A-2

Query Match 78.8%; Score 63; DB 5; Length 86;  
Best Local Similarity 84.6%; Pred. No. 0.0021;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSGS 13  
| | | | | | | | | |  
Db 33 YPYDVPDYASLG 45

RESULT 7  
US-10-028-247-2  
; Sequence 2, Application US/10028247  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Stanley  
; APPLICANT: Lathrop, Stephanie J.  
; APPLICANT: Longchamp, Pascal F.  
; APPLICANT: Whalen, Robert G.  
; APPLICANT: Maxygen, Inc.  
; TITLE OF INVENTION: Methods and Compositions for Developing Spore Display  
; FILE REFERENCE: 18097A-033520US  
; CURRENT APPLICATION NUMBER: US/10/028,247  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: US 60/214,161  
; PRIOR FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: US 09/892,208  
; PRIOR FILING DATE: 2001-06-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
; FEATURE:  
; OTHER INFORMATION: CotC27 including HALL epitope region  
US-10-028-247-2

Query Match 78.8%; Score 63; DB 7; Length 86;  
Best Local Similarity 84.6%; Pred. No. 0.0021;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSGS 13  
| | | | | | | | | |  
Db 33 YPYDVPDYASLG 45

RESULT 8  
US-09-740-876-1  
; Sequence 1, Application US/09740876  
; GENERAL INFORMATION:  
; APPLICANT: BRANELLEC, Didier  
; WALSH, Kenneth  
; ISNER, Jeffrey M.  
; DENEFELE, Patrice  
; TITLE OF INVENTION: VIRAL VECTORS AND THEIR USE FOR TREATING  
; HYPERPROLIFERATIVE DISORDERS, IN PARTICULAR RESTENOSIS  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: Mail Drop 3c43, P.O. Box 5093  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA

; ZIP: 19426-0997  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/740,876  
; FILING DATE: 21-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/723,726  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: FR 95-04234  
; FILING DATE: 31-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin F.  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: ST95022A-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610)454-3816  
; TELEFAX: (610)454-3808  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-740-876-1

Query Match 73.8%; Score 59; DB 6; Length 14;  
Best Local Similarity 83.3%; Pred. No. 0.0014;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSG 12  
| | | | | | | | | |  
Db 1 YPYDVPDYASLG 12

RESULT 9  
US-09-415-765A-57  
; Sequence 57, Application US/09415765A  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide  
; TITLE OF INVENTION: Libraries  
; FILE REFERENCE: A66900-1/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/415,765A  
; CURRENT FILING DATE: 1999-10-08  
; PRIOR APPLICATION NUMBER: 03/169,015  
; PRIOR FILING DATE: 1998-10-08  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 57  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-415-765A-57

Query Match 73.8%; Score 59; DB 5; Length 19;  
Best Local Similarity 83.3%; Pred. No. 0.0019;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSG 12  
| | | | | | | | | |  
Db 5 YPYDVPDYASLG 16

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RESULT 10
US-09-626-580B-57
; SEQUENCE 57, Application US/09626580B
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide
; FILE REFERENCE: A-66900-2/RMS
; CURRENT APPLICATION NUMBER: US/09/626,580B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 09/169,015
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 09/415,765
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-626-580B-57

Query Match          73.8%; Score 59; DB 5; Length 19;
Best Local Similarity 83.3%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSG 12
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Db 5 YPYDVPDYASLG 16

RESULT 11
US-09-626-581C-57
; SEQUENCE 57, Application US/09626581C
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide
; FILE REFERENCE: A-66900-3/RMS
; CURRENT APPLICATION NUMBER: US/09/626,581C
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/169,015
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 09/415,765
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-626-581C-57

Query Match          73.8%; Score 59; DB 5; Length 19;
Best Local Similarity 83.3%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSG 12
   | | | | | | | |
Db 5 YPYDVPDYASLG 16

RESULT 12
US-09-481-620A-34
; SEQUENCE 34, Application US/09481620A
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; GENERAL INFORMATION:
; APPLICANT: ARIAD Gene Therapeutics, Inc.
; TITLE OF INVENTION: Rapamycin Based Regulation of Biological Events
; FILE REFERENCE: 345B PCT
; CURRENT APPLICATION NUMBER: US/09/481,620A
; CURRENT FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 12CA5epitope--SV40NLS
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(26)
US-09-481-620A-34

Query Match          73.8%; Score 59; DB 6; Length 26;
Best Local Similarity 83.3%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSG 12
   | | | | | | | |
Db 5 YPYDVPDYASLG 16

RESULT 13
US-09-620-955B-31
; SEQUENCE 31, Application US/09620955B
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerif, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/09/620,955B
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-620-955B-31

Query Match          73.8%; Score 59; DB 6; Length 27;
Best Local Similarity 71.4%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSGK 14
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Db 1 YPYDVPDYASKDGK 14

RESULT 14
US-10-002-244-33
; SEQUENCE 33, Application US/10002244
; GENERAL INFORMATION:
; APPLICANT: ARIAD Gene Therapeutics, Inc.
; TITLE OF INVENTION: Use of Heterologous Transcription Factors in Gene Therapy
; FILE REFERENCE: 346B USC1
; CURRENT APPLICATION NUMBER: US/10/002,244
; CURRENT FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 68
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: psMTN3
US-10-002-244-33
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Query Match 73.8%; Score 59; DB 7; Length 27;
Best Local Similarity 83.3%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 YPYDVPDYAGSG 12
Db 5 YPYDVPDYASLG 16
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RESULT 15
US-09-481-620A-24
; Sequence 24, Application US/09481620A
; GENERAL INFORMATION:
; APPLICANT: ARIAD Gene Therapeutics, Inc.
; TITLE OF INVENTION: Rapamycin Based Regulation of Biological Events
; FILE REFERENCE: 345B PCT
; CURRENT APPLICATION NUMBER: US/09/481,620A
; CURRENT FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 12CA5eptlope--SV40NLS--2FHD5'
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(41)
US-09-481-620A-24
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Query Match 73.8%; Score 59; DB 6; Length 41;
Best Local Similarity 83.3%; Pred. No. 0.0044;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 YPYDVPDYAGSG 12
Db 5 YPYDVPDYASLG 16
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Search completed: April 11, 2002, 10:21:36
Job time: 446 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2002, 10:20:51 ; Search time 266.73 Seconds  
(Without alignments)  
13.533 Million cell updates/sec

Title: US-09-284-787-3

Perfect score: 75

Sequence: 1 SGSGYPYDPDYA 13

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Pending\_Patents\_AA\_Main:\*
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  - 12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep.\*
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  - 24: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	13	16 US-09-284-787-3	Sequence 3, Appli
2	67	89.3	17	11 US-08-787-738-51	Sequence 51, Appl
3	67	89.3	17	11 US-08-787-738B-51	Sequence 51, Appl
4	67	89.3	17	13 US-08-963-368-51	Sequence 51, Appl
5	67	89.3	18	16 US-09-285-912-136	Sequence 136, App
6	67	89.3	18	16 US-09-285-912A-136	Sequence 136, App
7	67	89.3	37	16 US-09-285-912-130	Sequence 130, App
8	67	89.3	37	16 US-09-285-912A-130	Sequence 130, App
9	67	89.3	38	16 US-09-285-912-68	Sequence 68, Appl

10	67	89.3	38	16	US-09-285-912A-68	Sequence 68, Appl
11	65	86.7	16	1	PCT-US00-09002-11	Sequence 11, Appl
12	65	86.7	16	1	PCT-US98-16887-7	Sequence 7, Appl
13	65	86.7	16	15	US-09-134-793-7	Sequence 7, Appl
14	65	86.7	16	15	US-09-134-793A-7	Sequence 4, Appl
15	65	86.7	16	17	US-09-300-639B-4	Sequence 4, Appl
16	65	86.7	16	18	US-09-459-113A-15	Sequence 15, Appl
17	65	86.7	16	19	US-09-514-673-15	Sequence 15, Appl
18	64.5	86.0	165	21	US-09-780-224A-13	Sequence 13, Appl
19	62	82.7	28	5	US-08-108-351-4	Sequence 4, Appl
20	62	82.7	225	11	US-08-756-693-8	Sequence 8, Appl
21	62	82.7	225	11	US-08-756-693A-8	Sequence 8, Appl
22	62	82.7	346	16	US-09-215-569B-8	Sequence 8, Appl
23	61	81.3	10	22	US-09-849-243-3	Sequence 3, Appl
24	61	81.3	11	10	US-08-628-829-17	Sequence 17, Appl
25	61	81.3	11	22	US-09-849-243-2	Sequence 2, Appl
26	61	81.3	12	20	US-09-608-958-46	Sequence 46, Appl
27	61	81.3	12	22	US-09-849-243-1	Sequence 1, Appl
28	61	81.3	21	7	US-08-361-811-127	Sequence 127, App
29	61	81.3	21	7	US-08-381-478-169	Sequence 169, App
30	61	81.3	21	9	US-08-535-025-169	Sequence 169, App
31	61	81.3	21	9	US-08-591-919-169	Sequence 169, App
32	61	81.3	21	9	US-08-592-007-169	Sequence 169, App
33	61	81.3	21	9	US-08-592-027-169	Sequence 169, App
34	61	81.3	21	9	US-08-592-131-169	Sequence 169, App
35	61	81.3	21	13	US-08-964-039-169	Sequence 169, App
36	61	81.3	80	18	US-09-457-568-18	Sequence 18, Appl
37	61	81.3	80	18	US-09-457-646-18	Sequence 18, Appl
38	61	81.3	80	19	US-09-516-065-18	Sequence 18, Appl
39	61	81.3	177	18	US-09-457-568-12	Sequence 12, Appl
40	61	81.3	177	18	US-09-457-646-12	Sequence 12, Appl
41	61	81.3	177	19	US-09-516-065-12	Sequence 12, Appl
42	61	81.3	224	1	PCT-US00-27237-36	Sequence 36, Appl
43	61	81.3	224	1	PCT-US00-27237-40	Sequence 40, Appl
44	61	81.3	224	1	PCT-US00-27237-44	Sequence 44, Appl
45	61	81.3	224	1	PCT-US00-27237-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1  
US-09-284-787-3  
; Sequence 3, Application US/09284787  
; GENERAL INFORMATION:  
; APPLICANT: Roche Diagnostics GmbH  
; TITLE OF INVENTION: Monoclonal Antibodies Against the Epitope YPYDVPDYA, A Process  
; TITLE OF INVENTION: Producing the Same and their Use  
; FILE REFERENCE: BMID9913US  
; CURRENT APPLICATION NUMBER: US/09/284,787  
; PRIOR FILING DATE: 1999-08-16  
; PRIOR FILING DATE: 1997-10-20  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human influenza virus  
US-09-284-787-3

Query Match 100.0%; Score 75; DB 16; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSGYPYDPDYA 13

Db 1 SGSGYPYDPDYA 13

RESULT 2

US-08-787-738-51

; Sequence 51, Application US/08787738  
; GENERAL INFORMATION:  
; APPLICANT: Nolan, Garry P  
; APPLICANT: Rothenburg, Michael S.  
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR  
; FILE REFERENCE: A-64259-1 correction  
; CURRENT APPLICATION NUMBER: US/08/787,738  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: 08/589,108  
; PRIOR FILING DATE: 1996-01-23  
; PRIOR APPLICATION NUMBER: 08/589,911  
; PRIOR FILING DATE: 1996-01-23  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.  
US-08-787-738-51

Query Match 89.3%; Score 67; DB 11; Length 17;  
Best Local Similarity 91.7%; Pred. No. 0.00068;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
Db 2 GGGYPYDVPDYA 13

RESULT 3  
US-08-787-738B-51  
; Sequence 51, Application US/08787738B  
; GENERAL INFORMATION:  
; APPLICANT: Nolan, Garry P  
; APPLICANT: Rothenburg, Michael S.  
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR  
; FILE REFERENCE: A-64259-1 correction  
; CURRENT APPLICATION NUMBER: US/08/787,738B  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: 08/589,108  
; PRIOR FILING DATE: 1996-01-23  
; PRIOR APPLICATION NUMBER: 08/589,911  
; PRIOR FILING DATE: 1996-01-23  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.  
US-08-787-738B-51

Query Match 89.3%; Score 67; DB 11; Length 17;  
Best Local Similarity 91.7%; Pred. No. 0.00068;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
Db 2 GGGYPYDVPDYA 13

RESULT 4  
US-08-963-368-51  
; Sequence 51, Application US/08963368  
; GENERAL INFORMATION:  
; APPLICANT: Nolan, Garry P

; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRA-CELLULAR  
; FILE REFERENCE: A-64260-2/DJB/RMS/DR  
; CURRENT APPLICATION NUMBER: US/08/963,368  
; CURRENT FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 08/589,108  
; PRIOR FILING DATE: 1996-01-23  
; PRIOR APPLICATION NUMBER: 08/589,911  
; PRIOR FILING DATE: 1996-01-23  
; PRIOR APPLICATION NUMBER: 08/789,333  
; PRIOR FILING DATE: 1997-01-23  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: epitope tag  
; OTHER INFORMATION: sequence.  
US-08-963-368-51

Query Match 89.3%; Score 67; DB 13; Length 17;  
Best Local Similarity 91.7%; Pred. No. 0.00068;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
Db 2 GGGYPYDVPDYA 13

RESULT 5  
US-09-285-912-136  
; Sequence 136, Application US/09285912  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES  
; FILE REFERENCE: A-66103-1/DJB/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/285,912  
; CURRENT FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: 60/080,444  
; PRIOR FILING DATE: 1998-04-02  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 136  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-285-912-136

Query Match 89.3%; Score 67; DB 16; Length 18;  
Best Local Similarity 91.7%; Pred. No. 0.00073;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
Db 2 GGGYPYDVPDYA 13

RESULT 6  
US-09-285-912A-136  
; Sequence 136, Application US/09285912A  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES  
; FILE REFERENCE: A-66103-1/DJB/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/285,912A  
; CURRENT FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: 60/080,444

; PRIOR FILING DATE: 1998-04-02  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 136  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-285-912A-136

Query Match 89.3%; Score 67; DB 16; Length 18;  
Best Local Similarity 91.7%; Pred. No. 0.00073;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | | | | | | | | | |  
Db 2 GGGYPYDVPDYA 13

RESULT 7  
US-09-285-912-130  
; Sequence 130, Application US/09285912  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES  
; FILE REFERENCE: A-66103-1/DJB/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/285,912  
; CURRENT FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: 60/080,444  
; PRIOR FILING DATE: 1998-04-02  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 130  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-285-912-130

Query Match 89.3%; Score 67; DB 16; Length 37;  
Best Local Similarity 91.7%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | | | | | | | | | |  
Db 11 GGGYPYDVPDYA 22

RESULT 8  
US-09-285-912A-130  
; Sequence 130, Application US/09285912A  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES  
; FILE REFERENCE: A-66103-1/DJB/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/285,912A  
; CURRENT FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: 60/080,444  
; PRIOR FILING DATE: 1998-04-02  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 130  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-285-912A-130

Query Match 89.3%; Score 67; DB 16; Length 37;  
Best Local Similarity 91.7%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
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Db 11 GGGYPYDVPDYA 22

RESULT 9  
US-09-285-912-68  
; Sequence 68, Application US/09285912  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES  
; FILE REFERENCE: A-66103-1/DJB/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/285,912  
; CURRENT FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: 60/080,444  
; PRIOR FILING DATE: 1998-04-02  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 68  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-285-912-68

Query Match 89.3%; Score 67; DB 16; Length 38;  
Best Local Similarity 91.7%; Pred. No. 0.0018;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
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Db 11 GGGYPYDVPDYA 22

RESULT 10  
US-09-285-912A-68  
; Sequence 68, Application US/09285912A  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES  
; FILE REFERENCE: A-66103-1/DJB/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/285,912A  
; CURRENT FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: 60/080,444  
; PRIOR FILING DATE: 1998-04-02  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 68  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-285-912A-68

Query Match 89.3%; Score 67; DB 16; Length 38;  
Best Local Similarity 91.7%; Pred. No. 0.0018;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | | | | | | | | | |  
Db 11 GGGYPYDVPDYA 22

RESULT 11

PCT-US00-09002-11  
; Sequence 11, Application PC/TUS0009002  
; GENERAL INFORMATION:  
; APPLICANT: Mayo Foundation for Medical Education and Research et al.  
; TITLE OF INVENTION: Anti-apoptotic fusion polypeptide  
; FILE REFERENCE: 150.195W01  
; CURRENT APPLICATION NUMBER: PCT/US00/09002  
; CURRENT FILING DATE: 2000-04-07  
; EARLIER APPLICATION NUMBER: US 60/128,021  
; EARLIER FILING DATE: 1999-04-06  
; EARLIER APPLICATION NUMBER: US 60/127,867  
; EARLIER FILING DATE: 1999-04-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pTAT-HA linker  
PCT-US00-09002-11

Query Match 86.7%; Score 65; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SGYPYDVPDYA 13  
Db 2 SGYPYDVPDYA 12

RESULT 12  
PCT-US98-16887-7  
; Sequence 7, Application PC/TUS9816887  
; GENERAL INFORMATION:  
; APPLICANT: Washington University  
; TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/16887  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/056,713  
; FILING DATE: 22-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 47275-PCT  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
PCT-US98-16887-7  
Query Match 86.7%; Score 65; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SGYPYDVPDYA 13  
Db 2 SGYPYDVPDYA 12  
RESULT 13  
US-09-134-793-7  
; Sequence 7, Application US/09134793  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; APPLICANT: Jessee, Joel A.  
; TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/134,793  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/056,713  
; FILING DATE: 22-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 47275  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-134-793-7

Query Match 86.7%; Score 65; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SGYPYDVPDYA 13  
Db 2 SGYPYDVPDYA 12  
RESULT 14  
US-09-134-793A-7  
; Sequence 7, Application US/09134793A  
; GENERAL INFORMATION:  
; APPLICANT: DOWDY, STEVEN F.

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; APPLICANT: JESSEE, JOEL A.
; TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM AND USE THEREOF
; FILE REFERENCE: 1742/47275
; CURRENT APPLICATION NUMBER: US/09/134,793A
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pTAT-HA linker
US-09-134-793A-7

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```

Query Match      86.7%; Score 65; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 3 SGYPYDVPDYA 13
   |||||
Db 2 SGYPYDVPDYA 12

```

```

RESULT 15
US-09-300-639B-4
; Sequence 4, Application US/09300639B
; GENERAL INFORMATION:
; APPLICANT: Steven F. Dowdy
; TITLE OF INVENTION: Methods for Transducing Fusion Molecules
; FILE REFERENCE: 48031
; CURRENT APPLICATION NUMBER: US/09/300,639B
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,380
; PRIOR FILING DATE: 1998-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of pTAT-HA plasmid linker sequence
US-09-300-639B-4

```

```

Query Match      86.7%; Score 65; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 SGYPYDVPDYA 13
   |||||
Db 2 SGYPYDVPDYA 12

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Search completed: April 11, 2002, 10:20:51  
Job time: 401 sec

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	71	94.7	34	6	US-09-896-915-8	Sequence 8, Appl	
2	67	89.3	17	6	US-09-916-940-51	Sequence 51, Appl	
3	67	89.3	17	7	US-10-096-550-51	Sequence 51, Appl	
4	67	89.3	19	5	US-09-415-765A-57	Sequence 57, Appl	
5	67	89.3	19	5	US-09-626-580B-57	Sequence 57, Appl	
6	67	89.3	19	5	US-09-626-581C-57	Sequence 57, Appl	
7	65	86.7	16	5	US-09-775-052A-15	Sequence 15, Appl	
8	65	86.7	16	6	US-09-775-052-15	Sequence 15, Appl	
9	61	81.3	224	6	US-09-453-234-36	Sequence 36, Appl	
10	61	81.3	224	6	US-09-453-234-40	Sequence 40, Appl	
11	61	81.3	224	6	US-09-453-234-44	Sequence 44, Appl	
12	61	81.3	224	6	US-09-453-234-46	Sequence 46, Appl	
13	61	81.3	224	6	US-09-453-234-48	Sequence 48, Appl	
14	61	81.3	224	6	US-09-453-234-52	Sequence 52, Appl	
15	61	81.3	224	6	US-09-453-234-76	Sequence 76, Appl	
16	61	81.3	224	6	US-09-453-234-78	Sequence 78, Appl	
17	61	81.3	224	6	US-09-453-234-82	Sequence 82, Appl	
18	61	81.3	224	6	US-09-453-234-84	Sequence 84, Appl	
19	61	81.3	224	6	US-09-453-234-88	Sequence 88, Appl	
20	61	81.3	224	6	US-09-453-234-90	Sequence 90, Appl	
21	61	81.3	226	6	US-09-453-234-38	Sequence 38, Appl	
22	61	81.3	226	6	US-09-453-234-42	Sequence 42, Appl	
23	61	81.3	226	6	US-09-453-234-50	Sequence 50, Appl	
24	61	81.3	226	6	US-09-453-234-72	Sequence 72, Appl	
25	61	81.3	226	6	US-09-453-234-74	Sequence 74, Appl	

; PRIOR APPLICATION NUMBER: US 08/589,911  
; PRIOR FILING DATE: 1996-01-23  
; PRIOR APPLICATION NUMBER: US 08/789,333  
; PRIOR FILING DATE: 1997-01-23  
; PRIOR APPLICATION NUMBER: US 08/787,738  
; PRIOR FILING DATE: 1997-01-23  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: epitope tag  
; OTHER INFORMATION: sequence.  
US-09-916-940-51

Query Match 89.3%; Score 67; DB 6; Length 17;  
Best Local Similarity 91.7%; Pred. No. 9.2e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GSGYPYDVPDYA 13  
| | | | | | | | | | | | | | |  
Db 2 GGGYPYDVPDYA 13

RESULT 3  
US-10-096-550-51  
; Sequence 51, Application US/10096550  
; GENERAL INFORMATION:  
; APPLICANT: Nolan, Garry P  
; APPLICANT: Rothenburg, Michael S.  
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR  
; TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES  
; FILE REFERENCE: A-64259-1 correction  
; CURRENT APPLICATION NUMBER: US/10/096,550  
; PRIOR FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 08/787,738  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: 08/589,108  
; PRIOR FILING DATE: 1996-01-23  
; PRIOR APPLICATION NUMBER: 08/589,911  
; PRIOR FILING DATE: 1996-01-23  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.  
US-10-096-550-51

Query Match 89.3%; Score 67; DB 7; Length 17;  
Best Local Similarity 91.7%; Pred. No. 9.2e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GSGYPYDVPDYA 13  
| | | | | | | | | | | | | | |  
Db 2 GGGYPYDVPDYA 13

RESULT 4  
US-09-415-765A-57  
; Sequence 57, Application US/09415765A  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide  
; TITLE OF INVENTION: Libraries  
; FILE REFERENCE: A66900-1/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/415,765A

; CURRENT FILING DATE: 1999-10-08  
; PRIOR APPLICATION NUMBER: 09/169,015  
; PRIOR FILING DATE: 1998-10-08  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 57  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-415-765A-57

Query Match 89.3%; Score 67; DB 5; Length 19;  
Best Local Similarity 91.7%; Pred. No. 0.0001;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GSGYPYDVPDYA 13  
| | | | | | | | | | | | | | |  
Db 2 GGGYPYDVPDYA 13

RESULT 5  
US-09-626-580B-57  
; Sequence 57, Application US/09626580B  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide  
; TITLE OF INVENTION: Libraries  
; FILE REFERENCE: A-66900-2/RMS  
; CURRENT APPLICATION NUMBER: US/09/626,580B  
; CURRENT FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 09/169,015  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 09/415,765  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 57  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-626-580B-57

Query Match 89.3%; Score 67; DB 5; Length 19;  
Best Local Similarity 91.7%; Pred. No. 0.0001;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GSGYPYDVPDYA 13  
| | | | | | | | | | | | | | |  
Db 2 GGGYPYDVPDYA 13

RESULT 6  
US-09-626-581C-57  
; Sequence 57, Application US/09626581C  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide  
; TITLE OF INVENTION: Libraries  
; FILE REFERENCE: A-66900-3/RMS  
; CURRENT APPLICATION NUMBER: US/09/626,581C  
; CURRENT FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 09/169,015  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 09/415,765  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0



; SEQ ID NO 57  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-626-581C-57

Query Match 89.3%; Score 67; DB 5; Length 19;  
Best Local Similarity 91.7%; Pred. No. 0.0001;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
Db 2 GGGYPYDVPDYA 13

RESULT 7  
US-09-775-052A-15  
; Sequence 15, Application US/09775052A  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052A  
; CURRENT FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052A-15

Query Match 86.7%; Score 65; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGYPYDVPDYA 13  
| | | | | | | | | |  
Db 2 SGYPYDVPDYA 12

RESULT 8  
US-09-775-052-15  
; Sequence 15, Application US/09775052  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 09/208,966  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/082,402  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052-15

Query Match 86.7%; Score 65; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGYPYDVPDYA 13  
| | | | | | | | | |  
Db 2 SGYPYDVPDYA 12

RESULT 9  
US-09-453-234-36  
; Sequence 36, Application US/09453234  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: GenPharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: US 60/157,415  
; PRIOR FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-453-234-36

Query Match 81.3%; Score 61; DB 6; Length 224;  
Best Local Similarity 83.3%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
Db 212 GESYPYDVPDYA 223

RESULT 10  
US-09-453-234-40  
; Sequence 40, Application US/09453234  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: GenPharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: US 60/157,415  
; PRIOR FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-4L  
US-09-453-234-40

Query Match 81.3%; Score 61; DB 6; Length 224;  
Best Local Similarity 83.3%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | |  
Db 212 GESYPYDVPDYA 223

RESULT 11  
US-09-453-234-44  
; Sequence 44, Application US/09453234  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: GenPharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: US 60/157,415  
; PRIOR FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-8L  
US-09-453-234-44

Query Match 81.3%; Score 61; DB 6; Length 224;  
Best Local Similarity 83.3%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | |  
Db 212 GESYPYDVPDYA 223

RESULT 12  
US-09-453-234-46  
; Sequence 46, Application US/09453234  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: GenPharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: US 60/157,415  
; PRIOR FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-10L  
US-09-453-234-46

Query Match 81.3%; Score 61; DB 6; Length 224;  
Best Local Similarity 83.3%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | |  
Db 212 GESYPYDVPDYA 223

RESULT 13  
US-09-453-234-48  
; Sequence 48, Application US/09453234  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: GenPharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: US 60/157,415  
; PRIOR FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 48  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-21L  
US-09-453-234-48

Query Match 81.3%; Score 61; DB 6; Length 224;  
Best Local Similarity 83.3%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | |  
Db 212 GESYPYDVPDYA 223

RESULT 14  
US-09-453-234-52  
; Sequence 52, Application US/09453234  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: GenPharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: US 60/157,415  
; PRIOR FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 52  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: M1-25L  
US-09-453-234-52

Query Match 81.3%; Score 61; DB 6; Length 224;  
Best Local Similarity 83.3%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | |  
Db 212 GESYPYDVPDYA 223

```

RESULT 15
US-09-453-234-76
; Sequence 76, Application US/09453234
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-16L
US-09-453-234-76

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Query Match      81.3%; Score 61; DB 6; Length 224;
Best Local Similarity 83.3%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      2 GSGYPDVPDYA 13
Db      212 GESYPDVPDYA 223

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Search completed: April 11, 2002, 10:21:36
Job time: 446 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2002, 10:14:10 ; Search time 53.05 Seconds  
(without alignments)  
12.567 Million cell updates/sec

Title: US-09-284-787-1

Perfect score: 55

Sequence: 1 YPYDVPDYA 9

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A\_Geneseq\_1101.\*
- 2: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*
- 10: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 12: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*
- 13: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 16: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 17: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*
- 18: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*
- 19: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 21: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*
- 23: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	9	15 AAR56545	Hal epitope tag.
2	55	100.0	9	16 AAR78372	Viral antigenic ep
3	55	100.0	9	17 AAW03654	HA-epitope tag. S
4	55	100.0	9	17 AAR92029	Hydrophilic peptid
5	55	100.0	9	18 AAW30296	Epitope for anti-H
6	55	100.0	9	18 AAW27094	Transforming growt
7	55	100.0	9	18 AAW00970	Haemagglutinin epi
8	55	100.0	9	18 AAW23660	pJG4-5 library pla
9	55	100.0	9	18 AAW08162	Purification tag o
10	55	100.0	9	18 AAW12385	Influenza virus ha
11	55	100.0	9	18 AAW01661	10-mer peptide tag

12	55	100.0	9	19 AAW81556	12CA5 epitope of m
13	55	100.0	9	19 AAW76742	Murine signalling
14	55	100.0	9	19 AAW66198	Influenza haemaggl
15	55	100.0	9	19 AAW80131	12CA5 epitope of h
16	55	100.0	9	19 AAW76408	Human PAR-2 12CA5
17	55	100.0	9	19 AAW61471	Influenza haemaggl
18	55	100.0	9	19 AAW50249	Haemagglutinin tag
19	55	100.0	9	19 AAW48632	Chimeric adenovira
20	55	100.0	9	19 AAW60082	Influenza virus ha
21	55	100.0	9	19 AAW60722	Peptide sequence o
22	55	100.0	9	19 AAW59450	Human influenza vi
23	55	100.0	9	19 AAW46333	Binding domain of
24	55	100.0	9	20 AAY31722	Haemagglutinin epi
25	55	100.0	9	20 AAY39621	CTLA-4 VLD CDR loo
26	55	100.0	9	20 AAY26291	FLAG peptide from
27	55	100.0	9	20 AAY06463	Haemagglutinin ant
28	55	100.0	9	20 AAY25085	HA-tag peptide. U
29	55	100.0	9	20 AAW92477	Murine signalling
30	55	100.0	9	20 AAW84206	Peptide comprising
31	55	100.0	9	20 AAW73373	Haemagglutinin epi
32	55	100.0	9	21 AAB29591	HA residues used i
33	55	100.0	9	21 AAB10960	Influenza haemaglu
34	55	100.0	9	21 AAB29434	HA tag, SEQ ID NO:
35	55	100.0	9	21 AAB29033	SNP detection meth
36	55	100.0	9	21 AAB15369	Influenza haemaggl
37	55	100.0	9	21 AAB22878	HA epitope, SEQ ID
38	55	100.0	9	21 AAY96185	Haemagglutinin epi
39	55	100.0	9	21 AAB14332	Influenza virus HA
40	55	100.0	9	21 AAY96884	C-terminal influen
41	55	100.0	9	21 AAB03561	Murine signalling
42	55	100.0	9	21 AAY93541	Amino acid sequenc
43	55	100.0	9	21 AAY87916	Influenza haemaggl
44	55	100.0	9	21 AAY79580	Haemagglutinin epi
45	55	100.0	9	22 AAB61542	12CA5 antibody pep

ALIGNMENTS

RESULT 1

AAR56545

ID AAR56545 standard; Protein; 9 AA.

XX AAR56545;

XX 18-MAR-1995 (first entry)

XX Hal epitope tag.

XX Max-interacting protein; plasmid pJG4-5; fusion protein;  
cancer; diagnosis; therapy.

XX Homo sapiens.

XX WO9417101-A.

XX 04-AUG-1994.

XX 29-DEC-1993; 93WO-US12643.

XX 29-JAN-1993; 93US-0011398.

XX (GEHO ) GEN HOSPITAL CORP.

XX Brent R, Zervos AS;

XX WPI; 1994-264033/32.

XX Max-interacting polypeptide and DNA encoding them - used as  
PT anticancer agents and to screen for agents which inhibit cellular  
proliferation

XX Disclosure; Page 43; 57pp; English.

XX A Max-interacting (Mxi) protein fusion protein with the SV40  
 CC nuclear localization sequence (AAR56544), the B42 acid blob  
 CC transcriptional activation domain and the HA1 epitope tag is  
 CC expressed from pJG4-5 -1. Mxi (and sense/antisense RNA) can be  
 CC delivered to e.g. bone marrow as therapeutic agents for cancer.  
 XX SQ Sequence 9 AA; Length 9; DB 15; Score 55; DB 15; Length 9;  
 Query Match 100.0%; Score 55; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YPYDVPDYA 9  
 Db 1 ypydvpdy 9  
 |||||

RESULT 2  
 ID AAR78372 standard; peptide; 9 AA.  
 AC AAR78372;  
 XX 16-APR-1996 (first entry)  
 DT  
 DE Viral antigenic epitope of Influenza virus haemagglutinin (12CA5).  
 KW Truncated; tobacco mosaic virus; TMV; movement protein; coat protein;  
 KW frame shift; mutation; in-frame stop codon; antigen; mammal;  
 KW viral vaccine; contraceptive; immune response; plant virus; insect.  
 XX Influenza virus.  
 OS  
 PN WO9521248-A1.  
 XX 10-AUG-1995.  
 PD  
 PF 03-FEB-1995; 95WO-US01467.  
 XX 03-FEB-1994; 94US-0192477.  
 PR  
 XX (SCRI ) SCRIPPS RES INST.  
 PA  
 PI Beachy RN, Fitch JH;  
 XX WPI; 1995-283768/37.  
 DR  
 XX Overprodn. of heterologous peptide in plants via tobacco mosaic  
 PT virus infection - in which the coat protein gene is modified by  
 PT insertion of heterologous sequence, partic. for producing viral  
 PT antigens for vaccines  
 PS Claim 10; Page 109; 157pp; English.

XX This sequence represents a viral antigenic epitope of Influenza virus  
 CC haemagglutinin. The DNA sequence encoding this antigen may be included  
 CC into a modified tobacco mosaic virus (TMV) coat protein gene or a  
 CC modified movement gene. The modified infectious clone is used to  
 CC transfect a plant which is then cultured such that the epitope may be  
 CC recovered from the leaves. The epitope coding sequences are included  
 CC into the coat protein or movement protein genes such that the translated  
 CC product contains one or more amino acids immediately adjacent to the  
 CC epitope that are readily treated chemically or enzymatically to release  
 CC the peptide epitope from the precursor protein. Recombinant viruses  
 CC containing modified movement or coat proteins may be used in the method  
 CC of the invention for the overproduction of heterologous proteins. The  
 CC method is esp. used for the production of peptides which cause an  
 CC antigenic response in mammals, partic. for use in viral vaccines, or  
 CC for generating a contraceptive immune response. The infectious clones  
 CC may encode coat proteins for other plant viruses, or proteins conferring  
 CC protection against insects and diseases.

XX SQ Sequence 9 AA;  
 Query Match 100.0%; Score 55; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YPYDVPDYA 9  
 Db 1 ypydvpdy 9  
 |||||

RESULT 3  
 ID AAW03654 standard; Peptide; 9 AA.  
 XX AAW03654;  
 AC  
 XX 22-FEB-1997 (first entry)  
 DT  
 DE HA-epitope tag.  
 DE  
 XX HA-epitope tag; affinity tag; FADD; Fas receptor; binding;  
 KW Fas-associating protein with novel death domain; apoptosis;  
 KW gene therapy; antibody; immunoassay; drug screening; diagnostic;  
 KW AIDS; antinflammatory; antitumour; cerebroprotective;  
 KW neuroprotective.  
 XX Synthetic.  
 OS  
 PN WO9631603-A2.  
 XX 10-OCT-1996.  
 PD  
 PF 28-FEB-1996; 96WO-US02857.  
 XX 18-MAY-1995; 95US-0443982.  
 PR 03-APR-1995; 95US-0416379.  
 XX (UNMI ) UNIV MICHIGAN.  
 PA  
 PI Dixit VM, O'Rourke K;  
 XX WPI; 1996-465026/46.  
 DR  
 XX FADD protein that binds to cytoplasmic region of Fas receptor - for  
 PT identifying inhibitors of Fas-associated apoptosis useful for  
 PT treating e.g. AIDS, leukaemia, stroke, etc  
 XX Example 1; Page 51; 96pp; English.

XX This HA-epitope tag peptide has been fused to a FADD protein  
 CC (Fas-associating protein with novel death domain, AAT39397), which  
 CC binds the cytoplasmic region of a Fas receptor, and modulates  
 CC apoptosis induced by activation of the receptor by ligand binding.  
 CC DNA encoding the tag is fused to the FADD gene by PCR, downstream  
 CC of a cytomegalovirus promoter-enhancer in plasmid pcDNA3HA-FADD.  
 CC The resulting fusion protein is expressed in Escherichia coli and  
 CC used in an assay to demonstrate in vivo association of FADD protein  
 CC and Fas receptor via death domains. FADD DNA may be used in gene  
 CC therapy, and FADD protein or a corresponding antibody may be used  
 CC to screen for agents modulating FADD pathway cellular functions  
 CC and Fas-associated apoptosis, for use in therapy of e.g. AIDS,  
 CC inflammation, leukaemia, myocardial infarction, degenerative  
 CC disease, etc.

XX SQ Sequence 9 AA;  
 Query Match 100.0%; Score 55; DB 17; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YPYDVDPDYA 9  
 |||||  
 Db 1 YPYDVDPDYA 9

## RESULT 4

AAR92029  
 ID AAR92029 standard; peptide; 9 AA.

XX AC AAR92029;

XX DT 29-MAY-1996 (first entry)

XX DE Hydrophilic peptide for epimorphin modification (1).

XX KW Epimorphin; human; mouse; wound; burn; epithelial tissue;  
 KW diagnosis; treatment; morphogenetic abnormality; cosmetic;  
 KW hair growth stimulator.

XX OS Synthetic.

XX PN EP698666-A2.

XX PD 28-FEB-1996.

XX PF 20-JUN-1995; 95EP-0304270.

XX PR 31-MAR-1995; 95JP-0099980.

XX PR 21-JUN-1994; 94JP-0162874.

XX PR 31-MAR-1995; 95JP-0099979.

XX PA (SUME ) SUMITOMO ELECTRIC IND CO.

XX PI Hirai Y, Koshida S, Oka Y;

XX DR WPI; 1996-118213/13.

XX PT Novel polypeptide containing an epimorphin functional domain - has

XX PT possible benefits in epithelial tissue treatments, e.g. burns and

XX PS for artificial organs

XX PS Claim 8; Page 57; 62pp; English.

XX CC New polypeptides contain a first portion of 5-99 amino acids joined  
 CC to a second portion contg. at least a functional domain of  
 CC epimorphin. The first portion may be selected from the peptides  
 CC given in AAR92029 to AAR92036. The second portion may be full-length  
 CC epimorphin (see AAR92037 to AAR92042 for human and mouse epimorphins).

XX CC Fragments of epimorphins given in AAT16083 to AAT16090 are used in the

XX CC prodn. of modified epimorphins.

XX CC The modified epimorphins are useful for the development of diagnosis

XX CC and treatment of morphogenetic abnormalities of epithelial tissue or

XX CC novel remedies for wounds, eg burns, after surgery and for artificial

XX CC organs. They may also be used as components of cosmetics, hair

XX CC growth stimulators, etc.

XX SQ Sequence 9 AA;

## RESULT 5

AAW30296  
 ID AAW30296 standard; Peptide; 9 AA.

AC AAW30296;

XX DT 14-APR-1998 (first entry)

XX DE Epitope for anti-HA tag monoclonal antibody.

XX KW Selective target cell activation; G protein-coupled receptor;  
 KW RASSL; gene therapy; cell proliferation; haemagglutinin; HA tag;  
 KW monoclonal antibody.

XX OS Synthetic.

XX PN WO9735478-A1.

XX PD 02-OCT-1997.

XX PF 25-MAR-1997; 97WO-US05334.

XX PR 26-MAR-1996; 96US-0622348.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Conklin BR;

XX DR WPI; 1997-502739/46.

XX PT Selective activation of target cell expressing modified G protein  
 PT coupled receptor - allows control of cellular proliferation,  
 PT especially for amplification of transfected cells in gene therapy  
 XX Example 1; Page 57; 117pp; English.

XX CC This peptide comprises an epitope for an anti-haemagglutinin (HA)  
 CC tag monoclonal antibody. It can be included in the sequence of a  
 CC recombinant G protein-coupled receptor that is activated superiorly  
 CC by a synthetic ligand, i.e. a RASSL (see AAW30298 and AAW30299), to  
 CC facilitate ease of detection and purification. RASSLs are used in  
 CC a novel method for selectively activating a target cell, providing  
 CC direct, selective control of cellular proliferation, especially for  
 CC amplification of transfected cells during gene therapy procedures.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 18; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YPYDVDPDYA 9

Db 1 YPYDVDPDYA 9

## RESULT 6

AAW27094

ID AAW27094 standard; peptide; 9 AA.

XX AC AAW27094;

XX DT 19-NOV-1997 (first entry)

XX DE Transforming growth factor-beta activated kinase epitope HA-TAK1.

XX KW TGF-beta; signal transduction; TGF-beta activated kinase;  
 KW MAPK kinase activator; AMK-1; bone morphogenetic protein; BMP;  
 KW protein kinase; epitope.

XX OS Synthetic.

XX PN JP09163990-A.

XX PD 24-JUN-1997.

PF 27-SEP-1996; 96JP-0256747.  
XX  
PR 24-JUL-1996; 96US-0685625.  
PR 29-SEP-1995; 95JP-0253549.  
XX  
PA (CHUS ) CHUGAI PHARM CO LTD.  
PA (UENO/) UENO N.  
XX  
XX WPI; 1997-380171/35.

DR DNA encoding transforming growth factor-beta-activated kinase, TAK-1  
PT - useful for studying the TGF-beta signal transmission system  
XX

PS Example 4; Page 8; 20pp; Japanese.

CC The present sequence represents an epitope, HA-TAK1, of transforming  
CC growth factor-beta (TGF-beta) activated kinase, TAK-1. The DNA  
CC encoding TAK-1 is used to produce the TAK-1 protein which is involved  
CC in the TGF-beta family signal transmission system. TAK-1, also known  
CC as activator of MAPK Kinase (AMK-1), is an enzyme which is activated  
CC by TGF-beta and bone morphogenetic protein (BMP) and activates MAPK  
CC kinase by phosphorylation.

XX Sequence 9 AA;

Query Match 100.0%; Score 55; DB 18; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9  
Db | | | | | | | | |  
1 ypydvdpdy 9

## RESULT 7

AAW00970  
ID AAW00970 standard; Peptide; 9 AA.

XX AAW00970;

DT 12-NOV-1997 (first entry)

DE Haemagglutinin epitope.

XX DNA binding protein; RNA binding protein; amphipathic peptide;  
KW acidic extension peptide; gene control; gene regulation;  
KW transcription; dominant negative protein; cancer; drug therapy;  
KW drug design; EAP; leucine zipper; haemagglutinin.

XX Synthetic.

XX WO9705249-A2.

XX 13-FEB-1997.

XX 31-JUL-1996; 96WO-US12590.

XX 31-JUL-1996; 96US-0001654.

XX 31-JUL-1995; 95US-0001654.

XX 29-MAY-1996; 96US-0018496.

XX (KRYL/) KRYLOV D.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (VINS/) VINSON C R.

XX Krylov D, Vinson CR;

XX WPI; 1997-145687/13.

XX New nucleic acid binding proteins - having an acidic amino acid  
PT sequence extension at the amino-terminus, to increase ability to  
PT regulate gene transcription, useful e.g. in cancer therapeutics

XX Claim 16; Page 58; 144pp; English.

PS This peptide sequence comprises a haemagglutinin epitope that can  
CC be attached to the N-terminus of a nucleic acid binding protein  
CC (NABP) such as a leucine zipper bZIP protein or BHLH protein.  
CC Claimed NABPs having an appended acidic extension peptide (see  
CC AAW00958-65) can regulate the function of a target nucleic acid or  
CC gene to which they are bound, and act as potent dominant-negative  
CC regulators of gene transcription, cell growth and cell proliferation.  
CC They can be used in cancer therapeutics, to treat diseases caused by  
CC eukaryotic microorganisms or by viruses, and as tools for drug  
CC development, rational drug design, and drug and gene therapies.

XX Sequence 9 AA;

Query Match 100.0%; Score 55; DB 18; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9  
Db | | | | | | | | |  
1 ypydvdpdy 9

## RESULT 8

AAW23660  
ID AAW23660 standard; Peptide; 9 AA.

XX AAW23660;

DT 10-OCT-1997 (first entry)

DE pJG4-5 library plasmid HA1 epitope tag.

XX Human; cell differentiation; survival; carcinoma; psoriasis;  
KW ubiquitination; p53; tumour suppressor; homeostasis; papilloma virus;  
KW epithelial cell; acne; ichthyosis; aphthous ulcer; hair growth;  
KW antibody; cell proliferation.

XX Synthetic.

XX WO9640767-A2.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US09040.

XX 07-JUN-1995; 95US-0484878.

XX (MITO-) MITOTIX INC.

XX Beer-Romero PL, Draetta G, Rolfe M;

XX WPI; 1997-087053/08.

XX E6AP-binding proteins and related nucleic acid - useful for  
PT modulating cell differentiation, survival etc., partic. for  
PT treatment and diagnosis of carcinoma, psoriasis, etc

PS Disclosure; Page 73; 83pp; English.

XX The present sequence represents the HA1 epitope tag of the pJG4-5  
CC library plasmid used during the isolation of the E6AP-binding proteins.  
CC E6AP mediates ubiquitination and so the inactivation of e.g. p53 tumour  
CC suppressor. The E6AP-binding protein is likely to be involved in normal  
CC cell homeostasis and in the pathogenesis of proliferative and  
CC differentiation disorders, e.g. regulation of gene expression or the  
CC cell cycle, modification of cell surface receptors, biogenesis of the  
CC ribosomes and DNA repair. The protein, which can optionally be  
CC generated in vivo by gene therapy, may be useful in treatment and  
CC prevention of papilloma virus infected transformed cells and carcinoma,



CC and may also be used to regulate epithelial cell processes more  
 CC generally, e.g. in cases of psoriasis, acne, ichthyosis, aphthous  
 CC ulcers. It may also be used to control wound healing, and inhibit growth  
 CC of hair. It can also be used to generate antibodies which are used in  
 CC immunoassays to determine the protein levels. The encoding nucleic acid  
 CC can be used to prepare recombinant proteins and oligonucleotides useful  
 CC as probes and primers for diagnostic detection of (mutant) mRNA for the  
 CC protein in (transformed) cells, also for antisense therapy. It can also  
 CC be used for the detection of mutations in EGAP-binding protein-encoding  
 CC genes, mis-expression of these genes or mis-incorporation of the protein  
 CC in a transcription regulatory complex containing EGAP can be used to  
 CC assess risk of disorders characterised by cell proliferation.  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 Db 1 ypydvpdy 9

RESULT 9  
 AAW08162  
 ID AAW08162 standard; Peptide; 9 AA.

AC AAW08162;

DT 26-AUG-1997 (first entry)

DE Purification tag of a TGF-beta fusion protein.

XX Transforming growth factor-beta fusion protein; wound healing;  
 XX artificial skin; surgery recovery time.

OS Synthetic.

XX WO9639430-A1.

XX 12-DEC-1996.

XX 05-JUN-1996; 96WO-US08973.

XX 06-JUN-1995; 95US-0470837.

XX (CHEU/) CHEUNG D T.

XX (HALL/) HALL F L.

XX (NIMN/) NIMNI M E.

XX (TUAN/) TUAN T.

XX (WULL/) WU L.

XX Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;

XX WPI; 1997-043065/04.

XX N-PSDB; AAT42766.

XX Prepn. of transforming growth factor-beta fusion protein - useful to  
 XX reduce surgery recovery time and to prepare artificial skin

XX Claim 5; Page 44; 59pp; English.

XX A novel transforming growth factor-beta (TGF-beta) fusion protein  
 XX comprises a purification tag and a TGF active fragment. The present  
 XX sequence represents a specifically claimed purification tag.  
 XX Additionally, the fusion protein may comprise proteinase-sensitive  
 XX linker sites and binding domain so the protein sequence may contain  
 XX some or all of the following elements: purification tag:proteinase  
 XX site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes  
 XX wound healing, and the fusion protein can be used to reduce surgery  
 XX recovery time and in the preparation of artificial skin. The inclusion

CC of a purification tag facilitates purification of the fusion protein.  
 CC The proteinase site is included to permit cleavage and release of the  
 CC purification tag after purification if desired. The extracellular  
 CC matrix binding site facilitates delivery of the fusion protein to the  
 CC desired site of action. Delivery of the TGF-beta to the site to be  
 CC treated reduces the amount of TGF-beta required to be administered to  
 CC be effective and reduces the concentration of circulating TGF-beta  
 CC which may result in undesirable effects.  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 Db 1 ypydvpdy 9

RESULT 10

AAW12385

ID AAW12385 standard; Peptide; 9 AA.

XX AAW12385;

DT 18-JUN-1997 (first entry)

DE Influenza virus haemagglutinin epitope tag.

XX Plasmid pPhox.TM; eukaryotic expression vector; transfected cell;

XX single chain antibody; sfv; molecular hook; haemagglutinin;

XX epitope tag.

XX Influenza virus.

XX WO9708186-A1.

XX 06-MAR-1997.

XX 23-AUG-1996; 96WO-US15819.

XX 24-AUG-1995; 95US-0518835.

XX (INVI-) INVITROGEN CORP.

XX Baytan A, Bernhard A, Chang M, Chesnut RD, Hoeffler JP;

XX WPI; 1997-179169/16.

XX Eukaryotic expression vector - for identification and separation of  
 XX transfected cells from total cell population

XX Example 1; Page 27; 83pp; English.

XX A DNA sequence encoding an influenza virus haemagglutinin (HA)  
 XX epitope tag (AAW12385) and the murine Ig kappa-chain V-J2-C region  
 XX signal peptide (AAW12384) was subcloned from a single chain antibody  
 XX (sfv) contg. vector (pCR3.2) as an EcoRV-Sali fragment and ligated  
 XX with EcoRV/Sali-digested pCR3.1.1. The resulting vector was used  
 XX in the construction of eukaryotic expression vector pPhox.TM (see  
 XX also AAT63235). Expression of the HA epitope tag allowed detection  
 XX of the expressed sfv by monoclonal antibody 12CA5. Vector pPhox.TM  
 XX is used in novel methods for the identification and isolation of  
 XX transfected eukaryotic cells.

XX Sequence 9 AA;

Query Match 100.0%; Score 55; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 ID AAW01661  
 DB 1 YPYDVPDYA 9

RESULT 11  
 AAW01661  
 ID AAW01661 standard; Peptide; 9 AA.

AC AAW01661;

XX 25-MAR-1997 (first entry)

XX 10-mer peptide tag derived from Influenza haemagglutinin.

XX monoclonal; recombinant; antibody; bispecific; antigenic site;  
 KW Fab fragment; complementary interactive domain; leucine zipper;  
 KW c-fos; c-jun; treatment; cancer; viral infection; primer; PCR;  
 KW polymerase chain reaction; amplification; peptide tag.

XX Synthetic.

XX US5582996-A.

XX 10-DEC-1996.

XX 04-DEC-1990; 90US-0622983.

XX 31-JUL-1992; 92US-0917074.

XX 04-DEC-1990; 90US-0622983.

XX 03-DEC-1991; 91WO-US09019.

XX 27-MAY-1994; 94US-0250656.

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX Curtis PJ;

XX WPI; 1997-042302/04.

XX BI-specific antibodies comprising two Fab fragments linked through

XX leucine zipper - useful to detect selected antigen or to treat

XX cancer and viral infections

XX Example 1; Column 10; 10pp; English.

XX Recombinant antibodies capable of binding to two different antigenic  
 CC sites, contain Fab fragments from the same or, pref., different  
 CC antibodies, which are brought into association by complementary  
 CC interactive domains, esp. leucine zipper domains, which have been  
 CC inserted into a region of the antibody heavy chain constant region.  
 CC Recombinant proteins c-fos Lz/Fab OKT2 and c-jun Lz/Fab OKT3 showed  
 CC little or no binding to normal lymphocytes when analysed individually  
 CC but bound very clearly to the cells when mixed to form a homodimeric  
 CC antibody. The labelled antibodies are useful for detecting a selected  
 CC antigen (bound by the first or second Fab) in a biological sample or  
 CC treatment of cancer and viral infections. AAW01661 is a 10-mer peptide  
 CC tag derived from Influenza haemagglutinin. DNA encoding the 10-mer was  
 CC cloned into lambda Hc2 to provide a peptide tag which will be present  
 CC on the heavy chain cloned into pHC2.

XX Sequence 9 AA;

Query Match 100.0%; Score 55; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 ID AAW01661  
 DB 1 YPYDVPDYA 9

RESULT 12  
 AAW81556  
 ID AAW81556 standard; peptide; 9 AA.

XX AAW81556;

XX 04-FEB-1999 (first entry)

XX 12CA5 epitope of mouse LIFR alpha-chain.

XX LIFR; leukaemia inhibitory factor; LIF; interspecies; chimeric;  
 KW haemopoietin domain; immunoglobulin; cytokine; interleukin;  
 KW colony-stimulating factor; mouse; epitope.

XX Mus sp.

XX WO9848011-A1.

XX 29-OCT-1998.

XX 21-APR-1998; 98WO-AU00282.

XX 21-APR-1997; 97AU-0006328.

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Layton MJ, Metcalf D, Nicola NA, Owczarek CM, Zhang Y;

XX WPI; 1998-609986/51.

XX New polypeptide containing haemopoietin domain and  
 CC immunoglobulin-like domain - also related nucleic acid, binds  
 CC cytokines, specifically leukaemia inhibitory factor, and is used to  
 CC treat inflammation

XX Example 1; Page 24; 58pp; English.

XX This represents an in-frame 12CA5 peptide epitope of the alpha chain of  
 CC mouse leukaemia inhibitory factor (LIF) receptor (LIFR). The invention  
 CC relates to interspecies LIFR alpha-chain chimeras. The chimeric  
 CC polypeptide comprises (i) a haemopoietin domain, linked, bound or  
 CC associated with (ii) an immunoglobulin (Ig)-like domain, such that the  
 CC chimera can bind cytokines. The chimeric polypeptide specifically binds  
 CC LIF, so is used to treat conditions that require antagonism of LIF,  
 CC specifically inflammation, but more generally may be designed to bind  
 CC other cytokines such as interleukins and colony-stimulating factors.

XX Sequence 9 AA;

Query Match 100.0%; Score 55; DB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9

DB 1 YPYDVPDYA 9

RESULT 13  
 AAW76742  
 ID AAW76742 standard; Protein; 9 AA.

XX AAW76742;

XX 15-JAN-1999 (first entry)

XX Murine signalling chimeric protein peptide #7.

XX Induction; intracellular aggregation; cytoplasmic tail; zeta chain;  
 KW T cell receptor/CD3 complex; signal; transcription; reporter gene;  
 KW homodimerization; Fas receptor; cell-specific apoptosis; Gall4; VP16;  
 KW heterodimerization; primer.

```

XX OS Mus sp.
XX XX US5830462-A.
XX PN 03-NOV-1998.
XX PD
XX PF 07-JUN-1995; 95US-0478386.
XX PR 14-FEB-1995; 95US-0388653.
XX PR 12-FEB-1993; 93US-0017931.
XX PR 16-JUL-1993; 93US-0092977.
XX PR 07-JAN-1994; 94US-0179748.
XX PR 11-FEB-1994; 94US-0196043.
XX PR 18-AUG-1994; 94US-0292597.
XX PR 07-JUN-1995; 95US-0478386.
XX XX (HARD ) HARVARD COLLEGE.
XX PA (STRD ) UNIV LELAND S STANFORD.
XX PA
XX PI Belshaw P, Crabtree GR, Schreiber SL, Spencer DM;
XX PI Wandless TJ;
XX XX WPI: 1998-609192/51.
XX DR N-PSDB; AAV62953.
XX DR
XX XX Inducing a biological process in a cell using ligand-induced gene
PT expression for e.g. cell death - using DNA construct encoding
PT ligand-binding domain and dimerisable protein domain
PT
XX PS Disclosure; Column 71-72; 95pp; English.
XX XX
XX CC AAW76736-W76764 are peptides used to design primers used in a novel
XX CC method for inducing a biological process in a cell. The method can be
XX CC used to induce the intracellular aggregation of the cytoplasmic tail of
XX CC the zeta chain of the T cell receptor/CD3 complex, leading to signalling
XX CC and transcription of a reporter gene. The method also has applications
XX CC for the homodimerization of the cytoplasmic tail of the Fas receptor,
XX CC leading to cell-specific apoptosis and for the heterodimerization of Gal4
XX CC and VP16, leading to direct transcription of a reporter gene.
XX XX
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
DB 1 YPYDVPDYA 9
|||||

RESULT 14
AAW66198
ID AAW66198 standard; Peptide; 9 AA.
XX AC AAW66198;
XX DT 21-DEC-1998 (first entry)
XX DE Influenza haemagglutinin epitope.
XX XX
XX KW Intein; reca; DNA repair enzyme; vaccine; vector; antigen;
XX KW open reading frame; haemagglutinin.
XX XX
XX OS Influenza virus.
XX PN WO9840394-A1.
XX PD 17-SEP-1998.
XX XX
XX PF 10-MAR-1998; 98WO-US04805.

```

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XX PR 13-MAR-1997; 97US-0816721.
XX XX (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
XX PA
XX PI Daugelet S, Jacobs WR;
XX XX WPI: 1998-520797/44.
XX DR
XX XX New vector constructs for selection of open reading frames -
PT comprise origin of replication and DNA sequences encoding selectable
PT marker, intein and regulatory elements for expression
XX XX
XX PS Disclosure; Fig 7; 83pp; English.
XX XX
XX CC This peptide comprises the influenza virus haemagglutinin epitope.
XX CC A synthetic oligonucleotide (see AAV07684) encoding the epitope has
XX CC been inserted into plasmid pYU8763 (see AAV07706), which contains DNA
XX CC encoding Mycobacterium tuberculosis reca intein (see also AAV07705)
XX CC inserted into an aph selectable marker gene and includes an
XX CC internal BglII site. E. coli transformants showed a high splicing
XX CC frequency. The invention provides novel vector constructs that
XX CC include a DNA sequence encoding an intein inserted into a
XX CC selectable marker gene such as aph. DNA of interest can be cloned
XX CC into a unique restriction site of the intein, and the vector used
XX CC as a vaccine or transformed into a vaccine vector. The vectors may
XX CC also be used in methods of selecting translated open reading frames
XX CC or genes, leading to the identification of protective antigens of
XX CC pathogenic organisms.
XX XX
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
DB 1 YPYDVPDYA 9
|||||

RESULT 15
AAW80131
ID AAW80131 standard; peptide; 9 AA.
XX AC AAW80131;
XX DT 15-DEC-1998 (first entry)
XX DE 12CA5 epitope of haemagglutinin.
XX XX
XX KW Haemagglutinin 12CA5 epitope; polyclonal rabbit antibody HA.11;
XX KW human betal-adrenergic receptor; betal-AR; transgene;
XX KW heart tissue-specific promoter; transgenic animal model;
XX KW heart muscle disease; heart failure.
XX XX
XX OS Synthetic.
XX PN WO9844092-A1.
XX PD 08-OCT-1998.
XX XX
XX PF 02-APR-1998; 98WO-US06791.
XX XX
XX PR 03-APR-1997; 97US-0041966.
XX XX
XX PA (UYTE-) UNIV TECHNOLOGY CORP.
XX XX
XX PI Bristow MR, Port JD;
XX XX WPI: 1998-557104/47.
XX XX

```

PT Transgenic mice as models for heart disease - having incorporated in  
PT their genome a heart tissue-specific promoter operatively linked to  
PT DNA coding for a beta-1-adrenergic receptor  
XX  
PS Example 1; Page 15; 40pp; English.  
XX  
CC The present sequence represents the 12CA5 epitope of haemagglutinin. It  
CC is recognised by the polyclonal rabbit antibody HA.11. The sequence was  
CC produced by annealing 2 primers encoding the present sequence. These  
CC were used to create a epitope tag at the end of human beta1-adrenergic  
CC receptor (beta1-AR) cDNA, which is used to create the transgene of the  
CC invention. The specification describes a transgenic animal, especially  
CC a mouse, which has incorporated into its genome a transgene comprising  
CC a heart tissue-specific promoter operatively linked to a coding  
CC sequence comprising beta1-AR, the transgene being expressed in at least  
CC the myocardium of the heart of the transgenic animal. The transgenic  
CC animal can be used as a model for heart muscle disease and heart failure  
CC in a mammal. The transgene can also be used for treating heart failure.  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YPYDVPDYA 9  
Db 1 ypydvpdya 9  
|||||||

Search completed: April 11, 2002, 10:15:43  
Job time: 93 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2002, 10:14:10 ; Search time 24.73 Seconds  
(without alignments)  
8.190 Million cell updates/sec

Title: US-09-284-787-1  
Perfect score: 55  
Sequence: 1 PPDVDPYA 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	9	1 US-08-011-398B-6	Sequence 6, Appl
2	55	100.0	9	1 US-08-090-148-2	Sequence 2, Appl
3	55	100.0	9	1 US-08-370-225-6	Sequence 6, Appl
4	55	100.0	9	1 US-08-167-982-1	Sequence 1, Appl
5	55	100.0	9	1 US-08-634-060-31	Sequence 31, Appl
6	55	100.0	9	1 US-08-464-051-6	Sequence 6, Appl
7	55	100.0	9	1 US-08-461-859-6	Sequence 6, Appl
8	55	100.0	9	1 US-08-470-837-28	Sequence 28, Appl
9	55	100.0	9	2 US-08-478-386A-19	Sequence 19, Appl
10	55	100.0	9	2 US-08-292-597-19	Sequence 19, Appl
11	55	100.0	9	2 US-08-462-498-6	Sequence 6, Appl
12	55	100.0	9	2 US-08-522-267A-60	Sequence 6, Appl
13	55	100.0	9	2 US-08-388-653-19	Sequence 19, Appl
14	55	100.0	9	2 US-08-473-985-19	Sequence 19, Appl
15	55	100.0	9	2 US-08-690-011A-17	Sequence 17, Appl
16	55	100.0	9	2 US-08-690-011A-49	Sequence 49, Appl
17	55	100.0	9	2 US-08-685-625A-4	Sequence 4, Appl
18	55	100.0	9	2 US-08-687-559-14	Sequence 14, Appl
19	55	100.0	9	2 US-08-700-846-11	Sequence 11, Appl
20	55	100.0	9	2 US-08-287-537B-3	Sequence 3, Appl
21	55	100.0	9	2 US-08-483-898-19	Sequence 19, Appl
22	55	100.0	9	3 US-09-087-716-19	Sequence 19, Appl
23	55	100.0	9	3 US-08-853-733B-28	Sequence 28, Appl
24	55	100.0	9	3 US-08-554-385-6	Sequence 6, Appl
25	55	100.0	9	3 US-08-518-835-6	Sequence 6, Appl
26	55	100.0	9	3 US-09-157-753-19	Sequence 19, Appl
27	55	100.0	9	3 US-09-157-230-19	Sequence 19, Appl

28	55	100.0	9	3 US-09-087-811-19	Sequence 19, Appl
29	55	100.0	9	3 US-08-968-747-12	Sequence 12, Appl
30	55	100.0	9	3 US-09-156-855-19	Sequence 19, Appl
31	55	100.0	9	3 US-09-030-613-36	Sequence 36, Appl
32	55	100.0	9	3 US-08-493-071-21	Sequence 21, Appl
33	55	100.0	9	4 US-09-158-010-19	Sequence 19, Appl
34	55	100.0	9	4 US-08-360-694-3	Sequence 3, Appl
35	55	100.0	9	4 US-09-087-647-19	Sequence 19, Appl
36	55	100.0	9	4 US-09-284-033-17	Sequence 17, Appl
37	55	100.0	9	4 US-09-053-293-1	Sequence 1, Appl
38	55	100.0	9	4 US-09-208-966-17	Sequence 17, Appl
39	55	100.0	9	4 US-09-100-802-17	Sequence 17, Appl
40	55	100.0	9	4 US-09-140-084-1	Sequence 1, Appl
41	55	100.0	9	4 US-09-382-950-8	Sequence 8, Appl
42	55	100.0	9	4 US-09-451-905-36	Sequence 36, Appl
43	55	100.0	9	4 US-09-382-736B-9	Sequence 9, Appl
44	55	100.0	9	5 PCT-US93-10069-6	Sequence 6, Appl
45	55	100.0	9	5 PCT-US94-10936-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-08-011-398B-6  
; Sequence 6, Application US/08011398B  
; Patent No. 5512473  
; GENERAL INFORMATION:  
; APPLICANT: Roger Brent  
; APPLICANT: Antonis S. Zervos  
; TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED  
; TITLE OF INVENTION: MOLECULES AND METHODS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/011,398B  
; FILING DATE: 29 JAN 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul T. Clark  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/160001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: amino acid  
; STRANDEDNESS: N/A  
; TOPOLOGY: linear  
; US-08-011-398B-6

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
|||||  
Db 1 YPYDVPDYA 9

RESULT 2  
US-08-090-148-2  
; Sequence 2, Application US/08090148  
; Patent No. 5534257  
; GENERAL INFORMATION:  
; APPLICANT: Mastico, Robert Allan  
; APPLICANT: Stockley, Peter George  
; APPLICANT: Talbot, Simon John  
; TITLE OF INVENTION: Antigen-Presenting Capsid with  
; TITLE OF INVENTION: Fusion MS2-Coat Protein  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rosenman & Colin  
; STREET: 575 Madison Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10022-2585

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5", 1.44Mb  
; COMPUTER: IBM PS2-486  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/090,148  
; FILING DATE: 08/11/93  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9101550.3  
; FILING DATE: 01/24/91  
; APPLICATION NUMBER: PCT/GB92/00124  
; FILING DATE: 01/22/92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nissenbaum, Israel  
; REGISTRATION NUMBER: 27,582  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 940-8636  
; TELEFAX: (212) 940-6404  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: NOT RELEVANT  
; MOLECULE TYPE: PEPTIDE  
US-08-090-148-2

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
|||||  
Db 1 YPYDVPDYA 9

RESULT 3  
US-08-370-225-6  
; Sequence 6, Application US/08370225  
; Patent No. 5580736  
; GENERAL INFORMATION:  
; APPLICANT: Brent, Roger  
; APPLICANT: Gyuris, Jenő  
; APPLICANT: Golemis, Erica  
; TITLE OF INVENTION: Interaction Trap System for Isolating  
; TITLE OF INVENTION: No. 5580736el Proteins  
; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
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; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/370,225  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,038  
; FILING DATE: 10/30/92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/143001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-370-225-6

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
|||||  
Db 1 YPYDVPDYA 9

RESULT 4  
US-08-167-982-1  
; Sequence 1, Application US/08167982  
; Patent No. 5698424  
; GENERAL INFORMATION:  
; APPLICANT: Mastico, Robert Allan  
; APPLICANT: Stockley, Peter George  
; TITLE OF INVENTION: CAPSID FORMING AND CYSTEINE  
; TITLE OF INVENTION: MODIFIED CHIMAERIC MS-2 COAT  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Graham & James LLP  
; STREET: 885 Third Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10022-4834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5", 1.44Mb  
; COMPUTER: IBM Pentium  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/167,982  
; FILING DATE: 01/03/95  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: UK 9114003.8  
 ; FILING DATE: 06/28/91  
 ; APPLICATION NUMBER: PCT/GB92/01159  
 ; FILING DATE: 06/26/92  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Reingold, Jesse  
 ; REGISTRATION NUMBER: 20,461  
 ; REFERENCE/DOCKET NUMBER: Mastico  
 ; TELEPHONE: (212) 848-1032  
 ; TELEFAX: (212) 688-2449  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 AMINO ACIDS  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: NOT RELEVANT  
 ; MOLECULE TYPE: PEPTIDE  
 US-08-167-982-1

Query Match 100.0%; Score 55; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 Db 1 YPYDVPDYA 9

RESULT 5  
 US-08-634-060-31  
 ; Sequence 31, Application US/08634060  
 ; Patent No. 5712136  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wickham, Thomas J.  
 ; APPLICANT: Kovesdi, Imre  
 ; APPLICANT: Rosvink, Petrus W.  
 ; TITLE OF INVENTION: ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY  
 ; TITLE OF INVENTION: THE ADENOVIRUS PENTON BASE PROTEIN  
 ; NUMBER OF SEQUENCES: 60  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Leydig, Volt & Mayer, Ltd.  
 ; STREET: Two Prudential Plaza, Suite 4900  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk.  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/634,060  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/303,162  
 ; FILING DATE: 08-SEP-1994  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Killyk, John Jr.  
 ; REGISTRATION NUMBER: 30763  
 ; REFERENCE/DOCKET NUMBER: 71602  
 ; TELEPHONE: (312) 616-5600  
 ; TELEFAX: (312) 616-5700  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown

; MOLECULE TYPE: peptide  
 US-08-634-060-31  
 Query Match 100.0%; Score 55; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 55; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 Db 1 YPYDVPDYA 9

RESULT 6  
 US-08-464-051-6  
 ; Sequence 6, Application US/08464051  
 ; Patent No. 5780262  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Roger Brent  
 ; APPLICANT: Antonis S. Zervos  
 ; TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED  
 ; TITLE OF INVENTION: MOLECULES AND METHODS  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM PS/2 Model 502 or 55SX  
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)  
 ; SOFTWARE: WordPerfect (Version 5.1)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/464,051  
 ; FILING DATE: 05 JUN 1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/011,398  
 ; FILING DATE: 29 JAN 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Paul T. Clark  
 ; REGISTRATION NUMBER: 30,162  
 ; REFERENCE/DOCKET NUMBER: 00786/160002  
 ; TELEPHONE: (617) 542-5070  
 ; TELEFAX: (617) 542-8906  
 ; TELEX: 200134  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9  
 ; TYPE: amino acid  
 ; STRANDEDNESS: N/A  
 ; TOPOLOGY: linear  
 US-08-464-051-6

Query Match 100.0%; Score 55; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 Db 1 YPYDVPDYA 9

RESULT 7  
 US-08-461-859-6  
 ; Sequence 6, Application US/08461859  
 ; Patent No. 5786169  
 ; GENERAL INFORMATION:

APPLICANT: Brent, Roger  
APPLICANT: Gyuris, Jeno  
APPLICANT: Golemis, Erica  
TITLE OF INVENTION: Interaction Trap System for Isolating  
TITLE OF INVENTION: No. 5786169e1 Proteins  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461.859  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION NUMBER: 08/370.225  
FILING DATE: January 9, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969.038  
FILING DATE: October 30, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Lech, Karen F.  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/143002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-461-859-6

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
|||||  
Db 1 YPYDVPDYA 9

RESULT 8  
US-08-470-837-28  
Sequence 28, Application US/08470837  
Patent No. 5800811  
GENERAL INFORMATION:  
APPLICANT: Nimni, Marcel E.  
APPLICANT: Hall, Frederick L.  
APPLICANT: Tuan, Tai-Lan  
APPLICANT: Wu, Lingtao  
APPLICANT: Cheung, David T.  
TITLE OF INVENTION: Transforming Growth Factor B Fusion  
TITLE OF INVENTION: and  
TITLE OF INVENTION: Their Use in Wound Healing  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchants & Gould  
STREET: 11150 Santa Monica Boulevard, Suite 400  
CITY: Los Angeles  
STATE: California

COUNTRY: USA  
ZIP: 90025-3395  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470.837  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Janice A.  
REGISTRATION NUMBER: 34,051  
REFERENCE/DOCKET NUMBER: 30630-1US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310-445-1140  
TELEFAX: 310-445-9031  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-470-837-28

Query Match 100.0%; Score 55; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
|||||  
Db 1 YPYDVPDYA 9

RESULT 9  
US-08-478-386A-19  
Sequence 19, Application US/08478386A  
Patent No. 5830462  
GENERAL INFORMATION:  
APPLICANT: Crabtree, Gerald R.  
APPLICANT: Schreiber, Stuart L.  
APPLICANT: Spencer, David M.  
APPLICANT: Wandless, Thomas J.  
APPLICANT: Belshaw, Peter  
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED  
TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
STREET: 26 Landsdowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478.386A  
FILING DATE: 07/JUN/1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Figg, E. Anthony  
REGISTRATION NUMBER: 27,195  
REFERENCE/DOCKET NUMBER: 2054-114A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 19:



SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-478-386A-19

Query Match 100.0%; Score 55; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 Db 1 YPYDVPDYA 9

RESULT 10  
 US-08-292-597-19  
 Sequence 19, Application US/08292597  
 Patent No. 5834266  
 GENERAL INFORMATION:  
 APPLICANT: Gerald R. Crabtree  
 APPLICANT: Schreiber, Stuart L.  
 APPLICANT: Spencer, David M.  
 APPLICANT: Wandless, Thomas J.  
 APPLICANT: Belshaw, Peter  
 TITLE OF INVENTION: Regulated Apoptosis  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
 STREET: 26 Landsdowne Street  
 CITY: Cambridge  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02139  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC/DOS/MS/DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/292,597  
 FILING DATE: 18/AUG/1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Figg, E. Anthony  
 REGISTRATION NUMBER: 27,195  
 REFERENCE/DOCKET NUMBER: 2054-108A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 783-6040  
 TELEFAX: (202) 783-6031  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-292-597-19

Query Match 100.0%; Score 55; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 Db 1 YPYDVPDYA 9

RESULT 11  
 US-08-462-498-6  
 Sequence 6, Application US/08462498  
 Patent No. 5852169  
 GENERAL INFORMATION:  
 APPLICANT: Roger Brent  
 APPLICANT: Antonis S. Zervos  
 TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED  
 TITLE OF INVENTION: MOLECULES AND METHODS  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM PS/2 Model 502 or 55SX  
 OPERATING SYSTEM: MS-DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/462,498  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/011,398  
 FILING DATE: 29 JAN 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Paul T. Clark  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 00786/160001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9  
 TYPE: amino acid  
 STRANDEDNESS: N/A  
 TOPOLOGY: linear  
 US-08-462-498-6

Query Match 100.0%; Score 55; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 Db 1 YPYDVPDYA 9

RESULT 12  
 US-08-922-267A-60  
 Sequence 60, Application US/08922267A  
 Patent No. 5861239  
 GENERAL INFORMATION:  
 APPLICANT: Kley, Patrick W.  
 APPLICANT: Moore, Karen J.  
 TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
 TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
 NUMBER OF SEQUENCES: 82  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/922,267A  
FILING DATE: 2-SEP-1997  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/829,553  
FILING DATE: 28-MAR-1997  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/631,200  
FILING DATE: 12-APR-1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-085  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
US-08-922-267A-60

Query Match 100.0%; Score 55; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
DB 1 YPYDVPDYA 9

RESULT 13  
US-08-388-653-19  
Sequence 19, Application US/08388653  
Patent No. 5869337  
GENERAL INFORMATION:  
APPLICANT: Crabtree, Gerald R.  
APPLICANT: Schreiber, Stuart L.  
APPLICANT: Spencer, David M.  
APPLICANT: Wandless, Thomas J.  
APPLICANT: Belshaw, Peter  
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED  
TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
STREET: 26 Landsdowne Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC/DOS/MS/DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,653  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,386

FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Figg, E. Anthony  
REGISTRATION NUMBER: 27,195  
REFERENCE/DOCKET NUMBER: 2054-114A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-388-653-19

Query Match 100.0%; Score 55; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
DB 1 YPYDVPDYA 9

RESULT 14  
US-08-473-985-19  
Sequence 19, Application US/08473985  
Patent No. 5871753  
GENERAL INFORMATION:  
APPLICANT: Crabtree, Gerald R.  
APPLICANT: Schreiber, Stuart L.  
APPLICANT: Spencer, David M.  
APPLICANT: Wandless, Thomas J.  
APPLICANT: Belshaw, Peter  
APPLICANT: Ho, Steffan  
TITLE OF INVENTION: Regulated Transcription of Targeted Genes and  
TITLE OF INVENTION: Other Biological Events  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/473,985  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/179,748  
FILING DATE: 07-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-SU 9863  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-473-985-19

Query Match 100.0%; Score 55; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9  
| | | | | | | | |  
Db 1 YPYDVDPDYA 9

RESULT 15  
US-08-690-011A-17  
; Sequence 17, Application US/086900011A  
; Patent No. 5942433  
; GENERAL INFORMATION:  
; APPLICANT: VINSON, Charles R.  
; APPLICANT: KRYLOV, Dmitry  
; TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN  
; TITLE OF INVENTION: INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A  
; TITLE OF INVENTION: CELLULAR PROTEIN  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10154-0053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/690,011A  
; FILING DATE: 31-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/001,654  
; FILING DATE: 31-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/018,496  
; FILING DATE: 29-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Serunian, Leslie A.  
; REGISTRATION NUMBER: 35,353.  
; REFERENCE/DOCKET NUMBER: 2026-4199US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)758-4800  
; TELEFAX: (212)751-6849  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-690-011A-17

Query Match 100.0%; Score 55; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9  
| | | | | | | | |  
Db 1 YPYDVDPDYA 9

Search completed: April 11, 2002, 10:14:43  
Job time: 33 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 11, 2002, 10:14:10 ; Search time 27.06 Seconds  
(without alignments)  
25.335 Million cell updates/sec

Title: US-09-284-787-1  
Perfect score: 55  
Sequence: 1 YPYDVPDYA 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	330	2 JQ2374	hemagglutinin - in
2	55	100.0	330	2 JQ2375	hemagglutinin - in
3	55	100.0	331	2 JQ2377	hemagglutinin - in
4	55	100.0	331	2 JQ2378	hemagglutinin - in
5	55	100.0	347	2 S52173	hemagglutinin - in
6	55	100.0	347	2 S52174	hemagglutinin - in
7	55	100.0	347	2 S52175	hemagglutinin - in
8	55	100.0	347	2 S52176	hemagglutinin - in
9	55	100.0	347	2 S52178	hemagglutinin - in
10	55	100.0	347	2 S52179	hemagglutinin - in
11	55	100.0	347	2 S52180	hemagglutinin - in
12	55	100.0	347	2 S52182	hemagglutinin - in
13	55	100.0	347	2 S52183	hemagglutinin - in
14	55	100.0	347	2 S52185	hemagglutinin - in
15	55	100.0	347	2 S52186	hemagglutinin - in
16	55	100.0	347	2 S52187	hemagglutinin - in
17	55	100.0	347	2 S52188	hemagglutinin - in
18	55	100.0	347	2 S52189	hemagglutinin - in
19	55	100.0	347	2 S52191	hemagglutinin - in
20	55	100.0	347	2 S52195	hemagglutinin - in
21	55	100.0	347	2 S52197	hemagglutinin - in
22	55	100.0	347	2 S52199	hemagglutinin - in
23	55	100.0	362	2 S38637	hemagglutinin - in
24	55	100.0	550	1 HMIVS2	hemagglutinin prec
25	55	100.0	550	1 HMIVS3	hemagglutinin prec
26	55	100.0	550	1 HMIVS7	hemagglutinin prec
27	55	100.0	550	1 HMIV80	hemagglutinin prec
28	55	100.0	550	1 HMIV33	hemagglutinin prec
29	55	100.0	550	1 HMIV89	hemagglutinin prec

30	55	100.0	550	1 HMIV98	hemagglutinin prec
31	55	100.0	550	1 HMIV15	hemagglutinin prec
32	55	100.0	550	1 HMIV86	hemagglutinin prec
33	55	100.0	550	2 JQ1153	hemagglutinin prec
34	55	100.0	550	2 JQ1154	hemagglutinin prec
35	55	100.0	550	2 JQ1155	hemagglutinin prec
36	55	100.0	550	2 JQ1156	hemagglutinin prec
37	55	100.0	565	1 HMIVE2	hemagglutinin prec
38	55	100.0	565	1 HMIVE4	hemagglutinin prec
39	55	100.0	566	1 HMIVH	hemagglutinin prec
40	55	100.0	566	1 HMIVHA	hemagglutinin prec
41	55	100.0	566	1 HMIVHM	hemagglutinin prec
42	55	100.0	566	1 HMIV6	hemagglutinin prec
43	55	100.0	567	1 HMIVV	hemagglutinin prec
44	54	98.2	565	1 HMIVE1	hemagglutinin prec
45	54	98.2	565	1 HMIVE5	hemagglutinin prec

ALIGNMENTS

RESULT 1  
JQ2374  
hemagglutinin - influenza A virus (strain SN1289)  
C:Species: Influenza A virus  
C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
C:Accession: JQ2374  
R:Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.  
J. Gen. Virol. 74, 2513-2518, 1993  
A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtain  
A:Reference number: JQ2369; MUID:94065682  
A:Accession: JQ2374  
A:Molecule type: mRNA  
A:Residues: 1-330 <ROC>  
A:Cross-references: GB:L20115  
A:Experimental source: subtype H3N2  
C:Superfamily: Influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 330;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 98 YPYDVPDYA 106

RESULT 2  
JQ2375  
hemagglutinin - influenza A virus (strain SN1389 and IN0190)  
C:Species: Influenza A virus  
C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
C:Accession: JQ2375; JQ2376  
R:Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.  
J. Gen. Virol. 74, 2513-2518, 1993  
A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtain  
A:Reference number: JQ2369; MUID:94065682  
A:Accession: JQ2375  
A:Molecule type: mRNA  
A:Residues: 1-330 <ROC>  
A:Cross-references: GB:L20119  
A:Experimental source: subtype H3N2  
C:Superfamily: Influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 330;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 98 YPYDVPDYA 106

```
RESULT 3
hemagglutinin - influenza A virus (strain SD0191)
C:Species: influenza A virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C:Accession: JQ2377
R:Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained
A:Reference number: JQ2377
A:Accession: JQ2377
A:Molecule type: mRNA
A:Residues: 1-331 <ROC>
A:Cross-references: GB:L20105
A:Experimental source: subtype H3N2
C:Superfamily: Influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9
Db 98 YPYDVDPDYA 106
|||||

RESULT 4
hemagglutinin - influenza A virus (strain HI0191)
C:Species: influenza A virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C:Accession: JQ2378
R:Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained
A:Reference number: JQ2378
A:Accession: JQ2378
A:Molecule type: mRNA
A:Residues: 1-331 <ROC>
A:Cross-references: GB:L20102
A:Experimental source: subtype H3N2
C:Superfamily: Influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9
Db 98 YPYDVDPDYA 106
|||||

RESULT 5
hemagglutinin - influenza A virus (fragment)
C:Species: influenza A virus
C:Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C:Accession: S52173; S52190; S52192; S52177; S52181; S52194; S52184; S52193
R:Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circula
A:Reference number: S52173
A:Molecule type: mRNA
A:Residues: 1-347 <ELL>
A:Cross-references: EMBL:246392; NID:g609020; PIDN:CAA86527.1; PID:g609021
A:Experimental source: isolate A/Beijing/32/92
A:Accession: S52190
A:Molecule type: mRNA
```

```
A:Residues: 1-347 <EL2>
A:Cross-references: EMBL:246410; NID:g609053; PIDN:CAA86545.1; PID:g609054
A:Experimental source: isolate A/Hong Kong/23/92
A:Accession: S52192
A:Molecule type: mRNA
A:Residues: 1-347 <EL3>
A:Cross-references: EMBL:246409; NID:g609057; PIDN:CAA86544.1; PID:g609058
A:Experimental source: isolate A/Hong Kong/34/90
A:Accession: S52177
A:Molecule type: mRNA
A:Residues: 1-134, 'K', 136-156, 'L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227
A:Cross-references: EMBL:246395; NID:g609027; PIDN:CAA86530.1; PID:g1228087
A:Experimental source: isolate A/England/269/93
A:Accession: S52181
A:Molecule type: mRNA
A:Residues: 1-134, 'K', 136-156, 'L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227
A:Cross-references: EMBL:246399; NID:g609035; PIDN:CAA86534.1; PID:g609036
A:Experimental source: isolate A/England/328/93
A:Accession: S52194
A:Molecule type: mRNA
A:Residues: 1-134, 'K', 136-156, 'L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227
A:Cross-references: EMBL:246414; NID:g609061; PIDN:CAA86549.1; PID:g609062
A:Experimental source: isolate A/Scotland/160/93
A:Accession: S52196
A:Molecule type: mRNA
A:Residues: 1-134, 'K', 136-156, 'L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227
A:Cross-references: EMBL:246415; NID:g609065; PIDN:CAA86550.1; PID:g609066
A:Experimental source: isolate A/Scotland/174/93
A:Accession: S52184
A:Molecule type: mRNA
A:Residues: 1-74, 'N', 76-120, 'T', 122-156, 'L', 158-173, 'F', 175-188, 'S', 190-200, 'K', 202-2
A:Cross-references: EMBL:246402; NID:g609041; PIDN:CAA86537.1; PID:g609042
A:Experimental source: isolate A/England/471/93
A:Accession: S52193
A:Molecule type: mRNA
A:Residues: 1-74, 'N', 76-120, 'T', 122-156, 'L', 158-173, 'F', 175-188, 'S', 190-200, 'K', 202-2
A:Cross-references: EMBL:246413; NID:g609059; PIDN:CAA86548.1; PID:g609060
A:Experimental source: isolate A/Scotland/142/93
C:Superfamily: Influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9
Db 98 YPYDVDPDYA 106
|||||

RESULT 6
hemagglutinin - influenza A virus (isolate A/Beijing/353/89) (fragment)
C:Species: influenza A virus
A:Variety: isolate A/Beijing/353/89
C:Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
C:Accession: S52174
R:Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circ
A:Reference number: S52173
A:Accession: S52174
A:Molecule type: mRNA
A:Residues: 1-347 <ELL>
A:Cross-references: EMBL:246391; NID:g609022; PIDN:CAA86526.1; PID:g609023
A:Experimental source: isolate A/Beijing/353/89
C:Superfamily: Influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 YPYDVDPDYA 9  
 DB 98 YPYDVDPDYA 106

RESULT 7  
 S52175  
 hemagglutinin - influenza A virus (isolate A/England/1/93) (fragment)  
 C:Species: Influenza A virus  
 A:Variety: Isolate A/England/1/93  
 C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
 C:Accession: S52175  
 R:Ellis, J.S.  
 submitted to the EMBL Data Library, October 1994  
 A:Description: Antigenic and genetic variation in the haemagglutinin of recently circula  
 A:Reference number: S52173  
 A:Accession: S52175  
 A:Molecule type: mRNA  
 A:Residues: 1-347 <ELL>  
 A:Cross-references: EMBL:246393; NID:g609024; PIDN:CAA86528.1; PID:g940547  
 A:Experimental source: isolate A/England/1/93  
 C:Superfamily: Influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 347;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9  
 DB 98 YPYDVDPDYA 106

RESULT 8  
 S52176  
 hemagglutinin - influenza A virus (isolate A/England/247/93) (fragment)  
 C:Species: Influenza A virus  
 A:Variety: Isolate A/England/247/93  
 C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
 C:Accession: S52176  
 R:Ellis, J.S.  
 submitted to the EMBL Data Library, October 1994  
 A:Description: Antigenic and genetic variation in the haemagglutinin of recently circula  
 A:Reference number: S52173  
 A:Accession: S52176  
 A:Molecule type: mRNA  
 A:Residues: 1-347 <ELL>  
 A:Cross-references: EMBL:246394; NID:g609025; PIDN:CAA86529.1; PID:g609026  
 A:Experimental source: isolate A/England/247/93  
 C:Superfamily: Influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 347;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9  
 DB 98 YPYDVDPDYA 106

RESULT 9  
 S52178  
 hemagglutinin - influenza A virus (isolate A/England/284/93) (fragment)  
 C:Species: Influenza A virus  
 A:Variety: Isolate A/England/284/93  
 C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
 C:Accession: S52178  
 R:Ellis, J.S.  
 submitted to the EMBL Data Library, October 1994  
 A:Description: Antigenic and genetic variation in the haemagglutinin of recently circula  
 A:Reference number: S52173  
 A:Accession: S52178

A:Molecule type: mRNA  
 A:Residues: 1-347 <ELL>  
 A:Cross-references: EMBL:246396; NID:g609029; PIDN:CAA86531.1; PID:g609030  
 A:Experimental source: isolate A/England/284/93  
 C:Superfamily: Influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 347;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9  
 DB 98 YPYDVDPDYA 106

RESULT 10  
 S52179  
 hemagglutinin - influenza A virus (isolate A/England/286/93) (fragment)  
 C:Species: Influenza A virus  
 A:Variety: Isolate A/England/286/93  
 C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
 C:Accession: S52179  
 R:Ellis, J.S.  
 submitted to the EMBL Data Library, October 1994  
 A:Description: Antigenic and genetic variation in the haemagglutinin of recently circ  
 A:Reference number: S52173  
 A:Accession: S52179  
 A:Molecule type: mRNA  
 A:Residues: 1-347 <ELL>  
 A:Cross-references: EMBL:246397; NID:g609031; PIDN:CAA86532.1; PID:g609032  
 A:Experimental source: isolate A/England/286/93  
 C:Superfamily: Influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 347;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9  
 DB 98 YPYDVDPDYA 106

RESULT 11  
 S52180  
 hemagglutinin - influenza A virus (isolate A/England/289/93) (fragment)  
 C:Species: Influenza A virus  
 A:Variety: Isolate A/England/289/93  
 C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
 C:Accession: S52180  
 R:Ellis, J.S.  
 submitted to the EMBL Data Library, October 1994  
 A:Description: Antigenic and genetic variation in the haemagglutinin of recently circ  
 A:Reference number: S52173  
 A:Accession: S52180  
 A:Molecule type: mRNA  
 A:Residues: 1-347 <ELL>  
 A:Cross-references: EMBL:246398; NID:g609033; PIDN:CAA86533.1; PID:g609034  
 A:Experimental source: isolate A/England/289/93  
 C:Superfamily: Influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 347;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVDPDYA 9  
 DB 98 YPYDVDPDYA 106

RESULT 12

S52182  
hemagglutinin - influenza A virus (isolate A/England/328/93) (fragment)  
C:Species: Influenza A virus  
A:Variety: isolate A/England/328/93  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52182  
R:Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating  
A:Reference number: S52173  
A:Accession: S52182  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:246400; NID:g609037; PIDN:CAA86535.1; PID:g609038  
A:Experimental source: isolate A/England/346/93  
C:Superfamily: influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
Db 98 YPYDVPDYA 106

RESULT 13  
S52183  
hemagglutinin - influenza A virus (isolate A/England/347/93) (fragment)  
C:Species: Influenza A virus  
A:Variety: isolate A/England/347/93  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52183  
R:Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating  
A:Reference number: S52173  
A:Accession: S52183  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:246401; NID:g609039; PIDN:CAA86536.1; PID:g609040  
A:Experimental source: isolate A/England/347/93  
C:Superfamily: influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
Db 98 YPYDVPDYA 106

RESULT 14  
S52185  
hemagglutinin - influenza A virus (isolate A/England/67/94) (fragment)  
C:Species: Influenza A virus  
A:Variety: isolate A/England/67/94  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52185  
R:Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating  
A:Reference number: S52173  
A:Accession: S52185  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:246403; NID:g609043; PIDN:CAA86538.1; PID:g609044  
A:Experimental source: isolate A/England/67/94  
C:Superfamily: influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
Db 98 YPYDVPDYA 106

RESULT 15  
S52186  
hemagglutinin - influenza A virus (isolate A/England/68/94) (fragment)  
C:Species: Influenza A virus  
A:Variety: isolate A/England/68/94  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52186  
R:Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating  
A:Reference number: S52173  
A:Accession: S52186  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:246404; NID:g609045; PIDN:CAA86539.1; PID:g609046  
A:Experimental source: isolate A/England/68/94  
C:Superfamily: influenza virus hemagglutinin

Query Match 100.0%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
Db 98 YPYDVPDYA 106

Search completed: April 11, 2002, 10:16:16  
Job time: 126 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 11, 2002, 10:14:50 ; Search time 18.1 Seconds  
(without alignments)  
18.231 Million cell updates/sec

Title: US-09-284-787-1  
Perfect score: 55  
Sequence: 1 YPYDVPDYA 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	55	100.0	249	1 HEMA_IAX31	P03438 influenza a
2	55	100.0	328	1 HEMA_IAXN6	P04664 influenza a
3	55	100.0	328	1 HEMA_IAXU7	P04663 influenza a
4	55	100.0	550	1 HEMA_IAXAN	P03441 influenza a
5	55	100.0	550	1 HEMA_IADH1	P12582 influenza a
6	55	100.0	550	1 HEMA_IADH2	P12583 influenza a
7	55	100.0	550	1 HEMA_IADH3	P12584 influenza a
8	55	100.0	550	1 HEMA_IADH4	P12585 influenza a
9	55	100.0	550	1 HEMA_IADH6	P12587 influenza a
10	55	100.0	550	1 HEMA_IADH7	P12588 influenza a
11	55	100.0	550	1 HEMA_IADHK	P43257 influenza a
12	55	100.0	550	1 HEMA_IADHL	P43258 influenza a
13	55	100.0	550	1 HEMA_IADHM	P43259 influenza a
14	55	100.0	550	1 HEMA_IAGHK	P43260 influenza a
15	55	100.0	550	1 HEMA_IAMES	P12589 influenza a
16	55	100.0	550	1 HEMA_IAXH2	P11133 influenza a
17	55	100.0	550	1 HEMA_IAXH3	P11134 influenza a
18	55	100.0	565	1 HEMA_IAXH4	P16994 influenza a
19	55	100.0	565	1 HEMA_IAXH5	P16995 influenza a
20	55	100.0	566	1 HEMA_IAXH6	P16996 influenza a
21	55	100.0	566	1 HEMA_IAXH7	P16997 influenza a
22	55	100.0	566	1 HEMA_IAXH8	P16998 influenza a
23	55	100.0	566	1 HEMA_IAXH9	P16999 influenza a
24	55	100.0	566	1 HEMA_IAXH1	P03449 influenza a
25	55	100.0	566	1 HEMA_IAXH2	P03439 influenza a
26	55	100.0	566	1 HEMA_IAXH3	P03436 influenza a
27	55	100.0	566	1 HEMA_IAXH4	P19106 influenza a
28	55	100.0	566	1 HEMA_IAXH5	P26139 influenza a
29	55	100.0	567	1 HEMA_IAXH6	P03435 influenza a
30	54	98.2	565	1 HEMA_IAXH7	P16995 influenza a
31	54	98.2	565	1 HEMA_IAXH8	P16999 influenza a
32	54	98.2	565	1 HEMA_IAXH9	P16996 influenza a
33	54	98.2	565	1 HEMA_IAXH1	P16997 influenza a

ALIGNMENTS

RESULT 1					
HEMA_IAX31					
ID HEMA_IAX31	STANDARD;	PRT;	249 AA.		
AC P03438;					
DT 21-JUL-1986 (Rel. 01, Created)					
DT 21-JUL-1986 (Rel. 01, Last sequence update)					
DT 20-AUG-2001 (Rel. 40, Last annotation update)					
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN]					
DE (FRAGMENT).					
GN HA.					
OS Influenza A virus (strain X-31).					
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;					
OC Influenza virus A and B group; Influenza A viruses;					
OC Influenza A virus.					
OX NCBI_TaxID=11489;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=81030852; PubMed=7421990;					
RA Gething M.-J., Byle J., Skehel J.J., Waterfield M.;					
RT "Cloning and DNA sequence of double-stranded copies of haemagglutinin genes from H2 and H3 strains elucidates antigenic shift and drift in human influenza virus.";					
RL Nature 287:301-306(1980).					
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.					
CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HA1 AND HA2) LINKED BY A DISULFIDE BOND.					
CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.					
DR PIR; A04051; HMIVH.					
DR PIR; A93233; A93233.					
DR HSP; P03437; 5HMG.					
DR InterPro: IPR001364; Hemagglutn.					
DR Pfam: PF00509; Hemagglutinin; 1.					
DR ProDom: PD000225; Hemagglutn; 1.					
KW Envelope protein; Hemagglutinin; Glycoprotein; Signal.					
FT SIGNAL 1 16					
FT CHAIN 17 >249					
FT CARBOHYD 24 24					
FT CARBOHYD 38 38					
FT CARBOHYD 54 54					
FT CARBOHYD 97 97					
FT CARBOHYD 181 181					
FT NON_TER 249 249					
SQ SEQUENCE 249 AA; 27373 MW; 9537AA970BB79183 CRC64;					

Query Match 100.0%; Score 55; DB 1; Length 249;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YPYDVPDYA 9  
Db 114 YPYDVPDYA 122  
RESULT 2

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HEMA_IAEN6
ID HEMA_IAEN6 STANDARD; PRT; 328 AA.
AC P04664;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HA1 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/England/878/69).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81194918; PubMed=6164798;
RA Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.;
RT "Antigenic drift in the hemagglutinin of the Hong Kong influenza
subtypes: correlation of amino acid changes with alterations in viral
antigenicity.";
RL J. Virol. 37:845-853(1981).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
CC
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CC
CC EMBL; K03335; AAA43184.1; -
CC InterPro: IPR001364; Hemagglutn.
CC Pfam: PF00509; Hemagglutinin; 1.
CC ProDom: PD000225; Hemagglutn; 1.
KW Envelope protein; Hemagglutinin; Glycoprotein.
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 328 328
SQ SEQUENCE 328 AA; 36072 MW; 9C3A86B3A8D56FE CRC64;

Query Match 100.0%; Score 55; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
| | | | | | | |
Db 98 YPYDVPDYA 106

RESULT 3
HEMA_IAQV7
ID HEMA_IAQV7 STANDARD; PRT; 328 AA.
AC P04663;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HA1 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Qu/7/70).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;

HEMA_IABAN
ID HEMA_IABAN STANDARD; PRT; 550 AA.
AC P03441; Q83961; Q83962;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Bangkok/1/79).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11325;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82033259; PubMed=6169840;
RA Both G.W., Sleigh M.J.;
RT "Conservation and variation in the hemagglutinins of Hong Kong
subtype influenza viruses during antigenic drift.";
RL J. Virol. 39:663-672(1981).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
```

CC CELL RECEPTORS AND FOR INITIATING INFECTION.  
 CC -I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
 CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
 CC -I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
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 CC  
 CC EMBL: J02092; AAA43182.1; -  
 CC PIR: A04052; HMIV6.  
 CC InterPro: IPR001364; Hemagglutn.  
 CC Pfam: PF00509; Hemagglutinin; 1.  
 CC ProDom: PD000225; Hemagglutn; 1.  
 CC Envelope protein; Hemagglutinin; Glycoprotein.  
 CC NON\_TER 1 1  
 CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.  
 CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.  
 CC CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 126 126 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC SEQUENCE 550 AA; 61699 MW; FBD2EC200689CBE5 CRC64;  
 SQ  
 Query Match 100.0%; Score 55; DB 1; Length 550;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YPYDVPDYA 9  
 |||||  
 DB 98 YPYDVPDYA 106  
 RESULT 5  
 HEMA\_IADH1 STANDARD; PRT; 550 AA.  
 AC P12582; Q84021; Q84022;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;  
 DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).  
 GN HA.  
 OS Influenza A virus (strain A/Duck/Hokkaido/5/77).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses;  
 OC Influenza A virus.  
 OX NCBI\_TaxID=11357;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87265458; PubMed=2440178;  
 RA Kida H., Kawakita Y., Naeye C.W., Webster R.G.;  
 RT "Antigenic and genetic conservation of H3 influenza virus in wild  
 RT ducks";  
 RL Virology 159:109-119(1987).  
 CC -I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
 CC CELL RECEPTORS AND FOR INITIATING INFECTION.  
 CC -I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
 CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
 CC -I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
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 CC  
 CC EMBL: J02092; AAA43182.1; -  
 CC PIR: A04052; HMIV6.  
 CC InterPro: IPR001364; Hemagglutn.  
 CC Pfam: PF00509; Hemagglutinin; 1.  
 CC ProDom: PD000225; Hemagglutn; 1.  
 CC Envelope protein; Hemagglutinin; Glycoprotein.  
 CC NON\_TER 1 1  
 CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.  
 CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.  
 CC CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 126 126 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC SEQUENCE 550 AA; 61699 MW; FBD2EC200689CBE5 CRC64;  
 SQ

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 CC  
 CC EMBL: M16737; AAA43143.1; -  
 CC PIR: A27813; HMIV77.  
 CC InterPro: IPR001364; Hemagglutn.  
 CC Pfam: PF00509; Hemagglutinin; 1.  
 CC ProDom: PD000225; Hemagglutn; 1.  
 CC Envelope protein; Hemagglutinin; Glycoprotein.  
 CC NON\_TER 1 1  
 CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.  
 CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.  
 CC CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC SEQUENCE 550 AA; 61705 MW; 7E7ACFE716FC969A CRC64;  
 SQ  
 Query Match 100.0%; Score 55; DB 1; Length 550;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YPYDVPDYA 9  
 |||||  
 DB 98 YPYDVPDYA 106  
 RESULT 6  
 HEMA\_IADH2 STANDARD; PRT; 550 AA.  
 AC P12583; Q84011;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;  
 DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).  
 GN HA.  
 OS Influenza A virus (strain A/Duck/Hokkaido/8/80).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses;  
 OC Influenza A virus.  
 OX NCBI\_TaxID=11358;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87265458; PubMed=2440178;  
 RA Kida H., Kawakita Y., Naeye C.W., Webster R.G.;  
 RT "Antigenic and genetic conservation of H3 influenza virus in wild  
 RT ducks";  
 RL Virology 159:109-119(1987).  
 CC -I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
 CC CELL RECEPTORS AND FOR INITIATING INFECTION.  
 CC -I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
 CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
 CC -I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
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 CC  
 CC EMBL: M16738; AAA43144.1; -  
 CC PIR: B27813; HMIV80.  
 CC InterPro: IPR001364; Hemagglutn.  
 CC Pfam: PF00509; Hemagglutinin; 1.  
 CC ProDom: PD000225; Hemagglutn; 1.  
 CC

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FT CARBOHYD 483 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 550 AA; 61577 MW; 6C30BF67CFDCB7DE CRC64;

Query Match 100.0%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.023; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 YPYDVPDYA 9
   |||||
Db 98 YPYDVPDYA 106

RESULT 8
HEMA_IADH4
ID HEMA_IADH4 STANDARD; PRT; 550 AA.
AC P12595; Q84013; Q84014;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hokkaido/7/82).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11360;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=87265458; PubMed=2440178;
RX Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
RT "Antigenic and genetic conservation of H3 influenza virus in wild
RT ducks";
RL Virology, 159:109-119(1987).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC
CC EMBL; M16740; AAA43146.1; -.
CC PIR; D27813; HMIV89.
CC InterPro: IPR001364; Hemagglutn.
CC Pfam; PF00509; Hemagglutinin; 1.
CC ProDom; PD000225; Hemagglutn; 1.
CC Envelope protein; Hemagglutinin; Glycoprotein.
CC NON_TER 1 1
CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC FT CARBOHYD 8 8 N-LINKED (GLCNAC... ) (POTENTIAL).
CC FT CARBOHYD 22 22 N-LINKED (GLCNAC... ) (POTENTIAL).
CC FT CARBOHYD 38 38 N-LINKED (GLCNAC... ) (POTENTIAL).
CC FT CARBOHYD 165 165 N-LINKED (GLCNAC... ) (POTENTIAL).
CC FT CARBOHYD 285 285 N-LINKED (GLCNAC... ) (POTENTIAL).
CC FT CARBOHYD 483 483 N-LINKED (GLCNAC... ) (POTENTIAL).
CC SQ SEQUENCE 550 AA; 61664 MW; A16B2CF8CBBD9D0 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.023; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 YPYDVPDYA 9
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Db 98 YPYDVPDYA 106

RESULT 9
HEMA_IADH6
ID HEMA_IADH6 STANDARD; PRT; 550 AA.
AC P12587; Q84017;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hokkaido/9/85).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hokkaido/9/85).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11362;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87265458; PubMed=2440178;
RA Kida H., Kawaoka Y., Naeye C.W., Webster R.G.;
RT "Antigenic and genetic conservation of H3 influenza virus in wild
RT ducks.";
RL Virology 159:109-119(1987).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC -----
CC EMBL; M16742; AAA43148.1; -
CC PIR; F27813; HMIV98.
CC InterPro: IPR001364; Hemagglutn.
CC Pfam: PF00509; Hemagglutinin; 1.
CC ProDom: PD000225; Hemagglutn; 1.
CC Envelope protein; Hemagglutinin; Glycoprotein.
CC NON_TER 1 1
CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CONFLICT 8 8 Y -> N (IN PIR DATA BANK).
CC SEQUENCE 550 AA; 61711 MW; 67BCD85F44736CFE CRC64;
SQ

Query Match 100.0%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
| | | | | | | |
Db 98 YPYDVPDYA 106

RESULT 10
HEMA_IADH7
ID HEMA_IADH7 STANDARD; PRT; 550 AA.
AC P12588; Q84018; Q89470;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)

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DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hokkaido/10/85).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11363;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87265458; PubMed=2440178;
RA Kida H., Kawaoka Y., Naeye C.W., Webster R.G.;
RT "Antigenic and genetic conservation of H3 influenza virus in wild
RT ducks.";
RL Virology 159:109-119(1987).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC -----
CC EMBL; M16743; AAA43149.1; -
CC PIR; G27813; HMIV15.
CC InterPro: IPR001364; Hemagglutn.
CC Pfam: PF00509; Hemagglutinin; 1.
CC ProDom: PD000225; Hemagglutn; 1.
CC Envelope protein; Hemagglutinin; Glycoprotein.
CC NON_TER 1 1
CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 550 AA; 61761 MW; 6EF81793281D53EB CRC64;
SQ

Query Match 100.0%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
| | | | | | | |
Db 98 YPYDVPDYA 106

RESULT 11
HEMA_IADHK
ID HEMA_IADHK STANDARD; PRT; 550 AA.
AC P43257;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hong Kong/7/75).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11364;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=91341491; PubMed=1875195;
RA Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
RT "Molecular evidence for a role of domestic ducks in the introduction
RT of avian H3 influenza viruses to pigs in southern China, where the
RT A/Hong Kong/68 (H3N2) strain emerged.";
RL J. Gen. Virol. 72:2007-2010(1991).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D00929; BAA00769.1; -.
DR HSP; P03437; 5HM.
DR InterPro; IPR001364; Hemagglutn.
DR Pfam; PF00509; Hemagglutinin; 1.
DR ProDom; PD000225; Hemagglutn; 1.
KW Envelope protein; Hemagglutinin; Glycoprotein.
FT NON_TER 1 1
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 550 AA; 61549 MW; 864639B829FE1BA9 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
DB 98 YPYDVPDYA 106
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RESULT 12
HEMA_IADHL STANDARD; PRT; 550 AA.
AC P43258;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hong Kong/64/76).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=45412;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91341491; PubMed=1875195;
RA Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
RT "Molecular evidence for a role of domestic ducks in the introduction
RT of avian H3 influenza viruses to pigs in southern China, where the
RT A/Hong Kong/68 (H3N2) strain emerged.";
RL J. Gen. Virol. 72:2007-2010(1991).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----

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CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC -----
DR EMBL; D00931; BAA00771.1; -.
DR HSP; P03437; 2HM.
DR InterPro; IPR001364; Hemagglutn.
DR Pfam; PF00509; Hemagglutinin; 1.
DR ProDom; PD000225; Hemagglutn; 1.
KW Envelope protein; Hemagglutinin; Glycoprotein.
FT NON_TER 1 1
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 550 AA; 61718 MW; A351C56789B4BE9A CRC64;

Query Match 100.0%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
DB 98 YPYDVPDYA 106
|||||

RESULT 13
HEMA_IADHM STANDARD; PRT; 550 AA.
AC P43259;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hong Kong/231/77).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=45412;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91341491; PubMed=1875195;
RA Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
RT "Molecular evidence for a role of domestic ducks in the introduction
RT of avian H3 influenza viruses to pigs in southern China, where the
RT A/Hong Kong/68 (H3N2) strain emerged.";
RL J. Gen. Virol. 72:2007-2010(1991).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC EMBL; D00932; BAA00772.1;
DR InterPro; IPR001364; Hemagglutn.
DR Pfam; PF00509; Hemagglutinin; 1.
DR ProDom; PD000225; Hemagglutn; 1.
KW Envelope protein; Hemagglutinin; Glycoprotein.
FT NON_TER 1
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 550 AA; 61762 MW; 6FEF8B49488C191A CRC64;

Query Match 100.0%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
DB 98 YPYDVPDYA 106

RESULT 14
HEMA_TAGHK
ID HEMA_TAGHK STANDARD; PRT; 550 AA.
AC F43260;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Goose/Hong Kong/10/76).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=45414;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91341491; PubMed=18751195;
RA Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
RT "Molecular evidence for a role of domestic ducks in the introduction
RT of avian H3 influenza viruses to pigs in southern China, where the
RT A/Hong Kong/68 (H3N2) strain emerged."
RL J. Gen. Virol. 72:2007-2010(1991).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC
CC EMBL; D00930; BAA00770.1;
DR HSSP; P03437; 5HMG.
DR InterPro; IPR001364; Hemagglutn.
DR Pfam; PF00509; Hemagglutinin; 1.
DR ProDom; PD000225; Hemagglutn; 1.
KW Envelope protein; Hemagglutinin; Glycoprotein.
FT NON_TER 1
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 550 AA; 61762 MW; 6FEF8B49488C191A CRC64;

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FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 550 AA; 61676 MW; 9A1E094DA28BACD2 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
DB 98 YPYDVPDYA 106

RESULT 15
HEMA_IAME6
ID HEMA_IAME6 STANDARD; PRT; 550 AA.
AC P12589;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Memphis/6/86).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11440;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88306236; PubMed=3407150;
RA Katz J.M., Webster R.G.;
RT "Antigenic and structural characterization of multiple subpopulations
RT of H3N2 influenza virus from an individual."
RL Virology 165:446-456(1988).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC
CC EMBL; M21648; AAA3275.1;
DR PIR; A29245; HMIV86.
DR HSSP; P03437; 2HMG.
DR InterPro; IPR001364; Hemagglutn.
DR Pfam; PF00509; Hemagglutinin; 1.
DR ProDom; PD000225; Hemagglutn; 1.
KW Envelope protein; Hemagglutinin; Glycoprotein.
FT NON_TER 1
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).

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SQ SEQUENCE 550 AA; 61804 MW; 52C9F14B309310ED CRC64;

Query Match 100.0%; Score 55; DB 1; Length 550;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
 |||||  
 Db 98 YPYDVPDYA 106

Search completed: April 11, 2002, 10:22:00  
 Job time: 430 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 11, 2002, 10:15:50 ; Search time 50.04 Seconds  
(without alignments)  
26.308 Million cell updates/sec

Title: US-09-284-787-1  
Perfect score: 55  
Sequence: 1 YPDVDPDYA 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: SP archaea.\*
  - 2: SP bacteria.\*
  - 3: SP fungi.\*
  - 4: SP human.\*
  - 5: SP invertebrate.\*
  - 6: SP mammal.\*
  - 7: SP mhc.\*
  - 8: SP organelle.\*
  - 9: SP phage.\*
  - 10: SP plant.\*
  - 11: SP rodent.\*
  - 12: SP virus.\*
  - 13: SP vertebrate.\*
  - 14: SP unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	236	12 Q9W821	Q9W821 influenza a
2	55	100.0	236	12 Q9W8T9	Q9W8T9 influenza a
3	55	100.0	236	12 Q9W8J7	Q9W8J7 influenza a
4	55	100.0	286	12 Q9W126	Q9W126 influenza a
5	55	100.0	286	12 Q9W125	Q9W125 influenza a
6	55	100.0	286	12 Q9W124	Q9W124 influenza a
7	55	100.0	325	12 Q40774	Q40774 influenza a
8	55	100.0	325	12 Q9DL45	Q9DL45 influenza a
9	55	100.0	326	12 Q40779	Q40779 influenza a
10	55	100.0	326	12 Q40780	Q40780 influenza a
11	55	100.0	327	12 Q92324	Q92324 influenza a
12	55	100.0	327	12 Q92325	Q92325 influenza a
13	55	100.0	327	12 Q92327	Q92327 influenza a
14	55	100.0	327	12 Q9Y190	Q9Y190 influenza a
15	55	100.0	327	12 Q9Y189	Q9Y189 influenza a
16	55	100.0	327	12 Q9Y188	Q9Y188 influenza a
17	55	100.0	327	12 Q9Y187	Q9Y187 influenza a
18	55	100.0	327	12 Q9Y186	Q9Y186 influenza a
19	55	100.0	327	12 Q9Y189	Q9Y189 influenza a

20	55	100.0	327	12 Q9YRU8	Q9YRU8 influenza a
21	55	100.0	327	12 Q9YRU7	Q9YRU7 influenza a
22	55	100.0	327	12 Q9YRU6	Q9YRU6 influenza a
23	55	100.0	327	12 Q9YRU5	Q9YRU5 influenza a
24	55	100.0	327	12 Q9YRU4	Q9YRU4 influenza a
25	55	100.0	327	12 Q9YRU3	Q9YRU3 influenza a
26	55	100.0	327	12 Q9YJ57	Q9YJ57 influenza a
27	55	100.0	327	12 Q9YIN9	Q9YIN9 influenza a
28	55	100.0	327	12 Q9Q884	Q9Q884 influenza a
29	55	100.0	328	12 Q40855	Q40855 influenza a
30	55	100.0	328	12 Q40867	Q40867 influenza a
31	55	100.0	328	12 Q82567	Q82567 influenza a
32	55	100.0	328	12 Q82568	Q82568 influenza a
33	55	100.0	328	12 Q82569	Q82569 influenza a
34	55	100.0	328	12 Q82578	Q82578 influenza a
35	55	100.0	328	12 Q82579	Q82579 influenza a
36	55	100.0	328	12 Q82580	Q82580 influenza a
37	55	100.0	328	12 Q82581	Q82581 influenza a
38	55	100.0	328	12 Q82575	Q82575 influenza a
39	55	100.0	328	12 Q82576	Q82576 influenza a
40	55	100.0	328	12 Q82577	Q82577 influenza a
41	55	100.0	328	12 Q82582	Q82582 influenza a
42	55	100.0	328	12 Q82583	Q82583 influenza a
43	55	100.0	328	12 Q82586	Q82586 influenza a
44	55	100.0	328	12 Q82587	Q82587 influenza a
45	55	100.0	328	12 Q82589	Q82589 influenza a

ALIGNMENTS

RESULT 1

Q9W821 ID Q9W821 PRELIMINARY; PRT; 236 AA.

AC Q9W821; RC STRAIN-TOKYO1527, TOKYO1511;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE HEMAGGLUTININ (FRAGMENT).

OS Influenza A virus.

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

OX Influenza virus A and B group; Influenza A viruses.

OX NCBI\_TaxID=11320;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-TOKYO1527, TOKYO1511;

RA Mori S., Sekine H.;

RT "HA1 domain of Influenza A (H3N2) virus.";

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB013807; BAA77285.1; -.

DR EMBL; AB013806; BAA77284.1; -.

DR InterPro; IPR001364; Hemagglutn.

DR Pfam; PF00509; Hemagglutinin; 1.

DR PRINTS; PR00329; HEMAGGLUTN12.

DR ProDom; PD000225; Hemagglutn; 1.

DR NON\_TER 1

FT NON\_TER 236

SQ SEQUENCE 236 AA; 26477 MW; 4566C8E7210FB558 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPDVDPDYA 9  
Db 11 YPDVDPDYA 19  
|||||

RESULT 2

Q9W8T9 ID Q9W8T9 PRELIMINARY; PRT; 236 AA.

AC Q9W8T9;

DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE HEMAGGLUTININ (FRAGMENT).  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TOKYO1570, TOKYO1566, TOKYO1567, TOKYO1568, TOKYO1569;  
RA Mori S., Sekine H.;  
RT "HAI domain of Influenza A (H3N2) virus.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB013813; BAA77291.1; -;  
DR EMBL; AB013809; BAA77287.1; -;  
DR EMBL; AB013810; BAA77288.1; -;  
DR EMBL; AB013811; BAA77289.1; -;  
DR EMBL; AB013812; BAA77290.1; -;  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.  
DR PRINTS; PR00329; HEMAGGLUTN12.  
DR ProDom; PD000225; Hemagglutn; 1.  
FT NON\_TER 1 236  
FT SEQUENCE 236 AA; 26491 MW; 44CDD257210FB558 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YPVDVDPYA 9  
Db 11 YPVDVDPYA 19  
|||||  
FT NON\_TER 1 236  
FT SEQUENCE 236 AA; 26491 MW; 44CDD257210FB558 CRC64;

RESULT 3  
Q9WBJ7 ID Q9WBJ7 PRELIMINARY; PRT; 236 AA.  
AC Q9WBJ7  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE HEMAGGLUTININ (FRAGMENT).  
GN HA.  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=70, AND 71;  
RA Nagashima M., Mori S., Sekine H.;  
RT "Influenza A virus gene for hemagglutinin.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TOKYO1539;  
RA Mori S., Sekine H.;  
RT "HAI domain of Influenza A (H3N2) virus.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB014062; BAA77294.1; -;  
DR EMBL; AB013808; BAA77286.1; -;  
DR EMBL; AB014060; BAA77292.1; -;  
DR EMBL; AB014061; BAA77293.1; -;  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.  
DR PRINTS; PR00329; HEMAGGLUTN12.  
DR ProDom; PD000225; Hemagglutn; 1.  
FT NON\_TER 1 236  
FT SEQUENCE 236 AA; 26493 MW; 457455682C8D28D7 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YPVDVDPYA 9  
Db 11 YPVDVDPYA 19  
|||||  
FT NON\_TER 1 236  
FT SEQUENCE 236 AA; 26491 MW; 44CDD257210FB558 CRC64;

RESULT 4  
Q9WI26 ID Q9WI26 PRELIMINARY; PRT; 286 AA.  
AC Q9WI26  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE H3 HEMAGGLUTININ (FRAGMENT).  
GN HA.  
OS Influenza A virus (A/Taiwan/2034/96(H3N2)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.  
OX NCBI\_TaxID=95241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/TAIWAN/2034/96;  
RA Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;  
RT "Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in Taiwan.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF139937; AAD34854.1; -;  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.  
DR PRINTS; PR00329; HEMAGGLUTN12.  
DR ProDom; PD000225; Hemagglutn; 1.  
FT NON\_TER 1 286  
FT SEQUENCE 286 AA; 32075 MW; 7BA39C7632D33186 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 286;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YPVDVDPYA 9  
Db 57 YPVDVDPYA 65  
|||||  
FT NON\_TER 1 286  
FT SEQUENCE 286 AA; 32075 MW; 7BA39C7632D33186 CRC64;

RESULT 5  
Q9WI25 ID Q9WI25 PRELIMINARY; PRT; 286 AA.  
AC Q9WI25  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE H3 HEMAGGLUTININ (FRAGMENT).  
GN HA.  
OS Influenza A virus (A/Taiwan/2192/96(H3N2)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.  
OX NCBI\_TaxID=95240;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/TAIWAN/2192/96;  
RA Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;  
RT "Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in Taiwan.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF139936; AAD34853.1; -;  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.  
FT NON\_TER 1 286  
FT SEQUENCE 286 AA; 32075 MW; 7BA39C7632D33186 CRC64;

DR PRINTS: PR00329; HEMAGGLUTININ2.  
DR ProDom: PD000225; Hemagglutn; 1.  
FT NON\_TER 1  
FT NON\_TER 286 286  
SQ SEQUENCE 286 AA; 32059 MW; CB51B092AAD0D7D8 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 286;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 57 YPYDVPDYA 65

RESULT 6  
Q9WI24 PRELIMINARY; PRT; 286 AA.

AC Q9WI24;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE H3 HEMAGGLUTININ (FRAGMENT).

GN HA.  
OS Influenza A virus (A/Taiwan/2191/96(H3N2)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.  
OX NCBI\_TaxID=95236;  
[1]

RP SEQUENCE FROM N.A.

RC STRAIN=A/TAIWAN/2191/96;

RA Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;

RT "Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in Taiwan";

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF139932; AAD34849.1; -

DR InterPro: IPR001364; Hemagglutn.

DR Pfam: PF00509; Hemagglutinin; 1.

DR PRINTS: PR00329; HEMAGGLUTIN2.

DR ProDom: PD000225; Hemagglutn; 1.

FT NON\_TER 1

FT NON\_TER 286 286

SQ SEQUENCE 286 AA; 31976 MW; 69AB2AE727D26078 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 286;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 57 YPYDVPDYA 65

RESULT 7  
O40774 PRELIMINARY; PRT; 325 AA.

AC O40774;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HEMAGGLUTININ GENE (FRAGMENT).

GN HA.

OS Influenza A virus.

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

OC Influenza virus A and B group; Influenza A viruses.

OX NCBI\_TaxID=11320;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=A/ILLINOIS/5/95(H3N2);

RA Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF008782; AAB63719.1; -  
DR InterPro: IPR001364; Hemagglutn.  
DR Pfam: PF00509; Hemagglutinin; 1.  
DR ProDom: PD000225; Hemagglutn; 1.  
FT NON\_TER 1  
FT NON\_TER 325 325  
SQ SEQUENCE 325 AA; 36103 MW; 4E5B4648C2024765 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 325;  
Best Local Similarity 100.0%; Pred. No. 0.073;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 98 YPYDVPDYA 106

RESULT 8  
Q9DL45 PRELIMINARY; PRT; 325 AA.

AC Q9DL45;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HEMAGGLUTININ (FRAGMENT).

OS Influenza A virus (A/Finland/583/98(H3N2)).

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.

OX NCBI\_TaxID=147149;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=A/FINLAND/583/98;

RA Pyhala R., Haanpää M., Kleemola M., Tervahauta R., Visakorpi R.,

RA Kinnunen L.;

RT "Acceptable protective efficacy of influenza vaccination in young

RT military conscripts in circumstances of incomplete antigenic and

RT genetic match.";

RL Vaccine 0:0-0(2001).

DR EMBL: AF3111689; AAG47810.1; -

DR InterPro: IPR001364; Hemagglutn.

DR Pfam: PF00509; Hemagglutinin; 1.

DR PRINTS: PR00329; HEMAGGLUTIN2.

DR ProDom: PD000225; Hemagglutn; 1.

FT NON\_TER 1

FT NON\_TER 325 325

SQ SEQUENCE 325 AA; 36029 MW; 5BECB8CC3E83B1C2 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 325;  
Best Local Similarity 100.0%; Pred. No. 0.073;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 98 YPYDVPDYA 106

RESULT 9  
O40779 PRELIMINARY; PRT; 326 AA.

AC O40779;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HEMAGGLUTININ GENE (FRAGMENT).

GN HA.

OS Influenza A virus.

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

OC Influenza virus A and B group; Influenza A viruses.

OX NCBI\_TaxID=11320;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=A/NEW\_YORK/28/94 (H3N2);  
 RA Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF008787; AAC63724.1; -;  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 FT NON\_TER 1  
 FT NON\_TER 326  
 SQ SEQUENCE 326 AA; 36197 MW; 4B84BD4AADC44A77 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 326;  
 Best Local Similarity 100.0%; Pred. No. 0.074;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 |||||  
 Db 98 YPYDVPDYA 106

RESULT 10  
 O40780  
 ID O40780 PRELIMINARY; PRT; 326 AA.  
 AC O40780;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEMAGGLUTININ GENE (FRAGMENT).  
 GN HA.  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses.  
 OX NCBI\_TaxID=11320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/PENNSYLVANIA/7/94 (H3N2);  
 RA Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF008788; AAC63725.1; -;  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 FT NON\_TER 1  
 FT NON\_TER 326  
 SQ SEQUENCE 326 AA; 36349 MW; 6A11A4CBBFBD6CC9 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 326;  
 Best Local Similarity 100.0%; Pred. No. 0.074;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 |||||  
 Db 98 YPYDVPDYA 106

RESULT 11  
 O92324  
 ID O92324 PRELIMINARY; PRT; 327 AA.  
 AC O92324;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEMAGGLUTININ (FRAGMENT).  
 GN HA.  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses.  
 OX NCBI\_TaxID=11320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/SYDNEY/05/97-LIKE (H3N2);

RA Osioy C.K.;  
 RT "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus  
 RT isolates circulating in Canada during the 1997/98 Influenza season.";  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF087700; AAC36729.1; -;  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 FT NON\_TER 1  
 FT NON\_TER 327  
 SQ SEQUENCE 327 AA; 36389 MW; 909239953649069E CRC64;

Query Match 100.0%; Score 55; DB 12; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 0.074;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 |||||  
 Db 98 YPYDVPDYA 106

RESULT 12  
 O92325  
 ID O92325 PRELIMINARY; PRT; 327 AA.  
 AC O92325;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEMAGGLUTININ (FRAGMENT).  
 GN HA.  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses.  
 OX NCBI\_TaxID=11320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/SYDNEY/05/97-LIKE (H3N2);  
 RA Osioy C.K.;  
 RT "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus  
 RT isolates circulating in Canada during the 1997/98 Influenza season.";  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF087703; AAC36732.1; -;  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 FT NON\_TER 1  
 FT NON\_TER 327  
 SQ SEQUENCE 327 AA; 36457 MW; D741E3C39D0C4D6A CRC64;

Query Match 100.0%; Score 55; DB 12; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 0.074; 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 |||||  
 Db 98 YPYDVPDYA 106

RESULT 13  
 O92327  
 ID O92327 PRELIMINARY; PRT; 327 AA.  
 AC O92327;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEMAGGLUTININ (FRAGMENT).  
 GN HA.  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses.  
 OX NCBI\_TaxID=11320;

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RN  SEQUENCE FROM N.A.
RP  STRAIN=A/SYDNEY/05/97(H3N2);
RA  "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
RT  Isolates circulating in Canada during the 1997/98 Influenza season.";
RL  Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AF087709; AAC36738.1; -.
DR  InterPro: IPR001364; Hemagglutn.
DR  Pfam: PF00509; Hemagglutinin; 1.
DR  ProDom: PD000225; Hemagglutn; 1.
FT  NON_TER 1
FT  NON_TER 327
SQ  SEQUENCE 327 AA; 36293 MW; 4A72007829B091F5 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
Db 98 YPYDVPDYA 106

RESULT 14
Q9YT90 PRELIMINARY; PRT; 327 AA.
AC Q9YT90;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HEMAGGLUTININ (FRAGMENT).
GN HA.
OS Influenza A virus (A/Sydney/05/97-like(H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=82372;
RN  SEQUENCE FROM N.A.
RP  STRAIN=A/SYDNEY/05/97-LIKE(H3N2);
RA  Osiowy C.K.;
RT  "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
RL  Isolates circulating in Canada during the 1997/98 Influenza season.";
DR  EMBL: AF087701; AAC36730.1; -.
DR  InterPro: IPR001364; Hemagglutn.
DR  Pfam: PF00509; Hemagglutinin; 1.
DR  PRINTS: PR00329; HEMAGGLUTN12.
DR  ProDom: PD000225; Hemagglutn; 1.
FT  NON_TER 1
FT  NON_TER 327
SQ  SEQUENCE 327 AA; 36373 MW; ADBD67D856EBC96 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
Db 98 YPYDVPDYA 106

RESULT 15
Q9YT89 PRELIMINARY; PRT; 327 AA.
AC Q9YT89;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HEMAGGLUTININ (FRAGMENT).
GN HA.

```

```

OS Influenza A virus (A/Sydney/05/97-like(H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=82372;
RN  SEQUENCE FROM N.A.
RP  STRAIN=A/SYDNEY/05/97-LIKE(H3N2);
RA  Osiowy C.K.;
RT  "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
RL  Isolates circulating in Canada during the 1997/98 Influenza season.";
DR  EMBL: AF087702; AAC36731.1; -.
DR  InterPro: IPR001364; Hemagglutn.
DR  Pfam: PF00509; Hemagglutinin; 1.
DR  PRINTS: PR00329; HEMAGGLUTN12.
DR  ProDom: PD000225; Hemagglutn; 1.
FT  NON_TER 1
FT  NON_TER 327
SQ  SEQUENCE 327 AA; 36446 MW; 9E9FA8433CFC1B01 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
Db 98 YPYDVPDYA 106

Search completed: April 11, 2002, 10:22:57
Job time: 427 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 11, 2002, 10:15:43 ; Search time 53.05 Seconds  
(without alignments)  
19.548 Million cell updates/sec

Title: US-09-284-787-2

Perfect score: 80

Sequence: 1 YPYDVPDAGSGSK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT.\*
- 2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 7: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT.\*
- 8: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT.\*
- 9: /SID8/gcgdata/geneseq/geneseq/AA1988.DAT.\*
- 10: /SID8/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 11: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT.\*
- 12: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT.\*
- 13: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT.\*
- 17: /SID8/gcgdata/geneseq/geneseq/AA1996.DAT.\*
- 18: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT.\*
- 19: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SID8/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT.\*
- 22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	14	AAW59451	Human influenza vl
2	75	93.8	165	AAW59451	Amino acid sequenc
3	71	88.8	34	AAW59451	Peptide encoded by
4	68	85.0	32	AAW59451	Peptide EL685Al f
5	67	83.0	481	AAW27158	Saccharomyces cere
6	65	81.2	16	AAW59451	PTAT-HA linker pol
7	65	81.2	16	AAW59451	PTAT-HA linker enc
8	65	81.2	17	AAW41032	Flu-epitope scamb
9	65	81.2	17	AAW29116	Flu-epitope tagged
10	65	81.2	17	AAW45969	Transdominant effe
11	65	81.2	25	AAW48631	Chimeric adenovira

12	65	81.2	25	19	AAW46332	Haemagglutinin seq
13	63	78.8	15	17	AAW81452	Haemagglutinin tag
14	62	77.5	228	21	AAW10433	Expression vector
15	62	77.5	232	20	AAW00874	PHOOK-1.GM-CSF fus
16	62	77.5	352	20	AAW06272	Anti-Fc gamma rece
17	62	77.5	353	20	AAW06273	Anti Fc alpha rece
18	61	76.2	12	19	AAW72791	HA tag. Synthetic
19	61	76.2	353	16	AAW81355	Thrombopoietin pro
20	61	76.2	353	16	AAW81356	Thrombopoietin pro
21	61	76.2	371	20	AAW73369	Epitope tagged TBP
22	60.5	75.6	272	17	AAW92254	Neural cell adhesi
23	60	75.0	2272	18	AAW21731	GALA/HA/NUMA fusio
24	59	73.8	14	17	AAW05097	HA1 epitope. Infl
25	59	73.8	18	20	AAW95558	Mus musculus haema
26	59	73.8	19	21	AAW90725	Influenza haemaggl
27	59	73.8	27	18	AAW08426	PSMTN3 fragment fo
28	59	73.8	27	20	AAW30054	Peptide encoded b
29	59	73.8	27	22	AAW69626	Plasma membrane ta
30	59	73.8	38	20	AAW49751	Compact structure
31	59	73.8	41	18	AAW08425	Construct pCGNN-2F
32	59	73.8	181	21	AAW21192	Exo16 partial prot
33	59	73.8	359	20	AAW85003	Amino acid sequenc
34	59	73.8	359	21	AAW86206	LexA-GALA fusion p
35	59	73.8	389	21	AAW96709	HA-Tagged I-kappa-
36	59	73.8	971	16	AAW76070	Yeast MSH1 protein
37	58	72.5	20	21	AAW96145	CSFV envelope prot
38	58	72.5	126	20	AAW32764	HM1.24 antigenic p
39	58	72.5	143	20	AAW32763	HM1.24 antigenic p
40	58	72.5	147	20	AAW32768	HM1.24 antigenic p
41	58	72.5	1070	18	AAW17789	Green fluorescent
42	57	71.2	13	19	AAW44013	Haemagglutinin pep
43	57	71.2	13	22	AAW30796	Amino acid sequenc
44	57	71.2	21	21	AAW49277	Sequence of angios
45	57	71.2	27	21	AAW49279	Sequence of angios

#### ALIGNMENTS

##### RESULT 1

AAW59451

ID AAW59451 standard; peptide; 14 AA.

AC AAW59451;

DT 28-AUG-1998 (first entry)

DE Human influenza virus haemagglutinin epitope peptide fragment #2.

KW Haemagglutinin; epitope; monoclonal antibody; detection; isolation;

KW fusion protein.

OS Human parainfluenza virus.

PH Key Location/Qualifiers

FT Modified-site 1 /note- "N-terminal acetyl group"

FT Modified-site 14

FT /note- "C-terminal epsilon-blonoyl-amide group"

PN DE19643314-Al.

PD 23-APR-1998.

PF 21-OCT-1996; 96DE-1043314.

PR 21-OCT-1996; 96DE-1043314.

PA (BOEF ) BOEHRINGER MANNHEIM GMBH.

PI Emrich T, Grol M, Hinzpeter M;

XX WPI; 1998-241603/22.

XX Monoclonal antibodies to Influenza virus haemagglutinin - useful for  
PT detecting and isolating haemagglutinin proteins  
XX  
XX Claim 7; Page 2; 6pp; German.  
XX  
CC This peptide fragment represents a human influenza virus haemagglutinin  
CC epitope which is used to make monoclonal antibodies with an affinity  
CC constant of 10<sup>8</sup> M-1. Such antibodies are used for detecting and isolating  
CC native human influenza virus haemagglutinin (HA), modified HA or HA  
CC fusion proteins.

XX Sequence 14 AA;  
SQ

Query Match 100.0%; Score 80; DB 19; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGSGSK 14  
Db 1 ypydvpdyagsgsk 14  
|||||

RESULT 2  
AAG63605 ,  
ID AAG63605 standard; Protein; 165 AA.  
AC AAG63605;  
XT DT 15-OCT-2001 (first entry)  
DE XX Amino acid sequence of N-terminal fusion protein of pIX protein.  
KW pIX protein; chimeric protein; gene transfer vector.  
OS Synthetic.  
OS Mastadenovirus.  
PN WO200158940-A2.  
XX WO200158940-A2.  
XX PD 16-AUG-2001.  
PF PF 09-FEB-2001; 2001WO-US04233.  
XX PR 09-FEB-2000; 2000US-0181163.  
XX PA (GENV-) GENVEC INC.  
PI Roelvink PW, Kovesdi I, Wickham TJ;  
XX WPI; 2001-497066/54.  
DR DR N-PSDB; AAH74658.  
XX  
XX Chimeric pIX protein useful in an adenovirus gene transfer vector for  
PT infecting cells comprises at least one adenoviral pIX domain and a  
PT non-native amino acid .  
XX Example 1; Page 26-27; 28pp; English.  
XX The present sequence represents a chimeric fusion protein of the  
CC invention. The specification describes a chimeric pIX protein having  
CC at least one adenoviral pIX domain and a non-native amino acid sequence.  
CC The non-native sequence is a ligand that binds to a substrate present on  
CC surface cells. The chimeric proteins are used for producing adenovirus  
CC gene transfer vectors.  
XX Sequence 165 AA;  
SQ

Query Match 93.8%; Score 75; DB 22; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX DE Peptide E16853A1 for construction of rTether1 containing HA-tag.  
 XX KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
 KW KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.  
 XX OS Synthetic.  
 XX XX WO200039278-A2.  
 XX PN 06-JUL-2000.  
 XX PD 30-DEC-1999; 99WO-US311108.  
 XX PF 31-DEC-1998; 98US-0114577.  
 XX PR (GARD/) GARDELLA T J.  
 XX PA (KRON/) KRONENBERG H M.  
 XX PA (POTT/) POTTS J T.  
 XX PA (JUEP/) JUEPPNER H.  
 XX PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX PS WPI: 2000-452384/39.  
 XX DR N-PSDB; AA51743.  
 XX XX New compound comprising an amino terminal signaling functional domain  
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
 PT treating mammalian conditions characterized by decreases in bone mass  
 XX Example 4; Fig 11G; 119pp; English.  
 XX CC AAA51738-44 were used to construct a chimeric rat PTH-1 receptor,  
 CC rTether1 and control plasmids.  
 CC Compounds of the structure or formula S-(L)<sub>n</sub>-B, R<sub>1</sub>-S-(L)<sub>n</sub>-R or  
 CC S-(L)<sub>n</sub>-R, are new. S is an amino terminal signaling functional domain  
 CC of parathyroid hormone (PTH); L is a linker molecule present n times  
 CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal  
 CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);  
 CC R<sub>1</sub> is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1  
 CC receptor sequence. The new compounds are used for treating mammalian  
 CC conditions characterized by decreases in bone mass, determining rates of  
 CC bone reformation, bone resorption and/or bone remodeling, treating  
 CC diseases and disorders associated with decreased tether1 activity,  
 CC increasing cAMP in a mammalian cell having PTH-1 receptors, or screening  
 CC for a peptide or non-peptide PTH (claimed). The new compound can be  
 CC administered by inhalation unlike the large native PTH or PTH-rp which  
 CC avoids the need for regular injections to treat osteoporosis.  
 XX XX Sequence 32 AA;  
 SQ

Query Match 85.0%; Score 68; DB 21; Length 32;  
 Best Local Similarity 78.6%; Pred. No. 0.00049;  
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 YPVDVDPYAGSGK 14  
 Db 10 ypydvpdyagggge 23  
 RESULT 5  
 AAW27158  
 ID AAW27158 standard; Protein: 481 AA.  
 XX AC AAW27158;  
 XX XX 20-APR-1998 (first entry)  
 DT  
 XX Saccharomyces cerevisiae alpha mating factor receptor Ste2.  
 DE Alpha mating factor receptor; Ste2; mutant; biosensor; diagnosis;  
 KW G-protein coupled receptor; GPCR; environmental monitoring;  
 KW

on-line process monitoring.  
 Saccharomyces cerevisiae.  
 WO9735985-A1.  
 02-OCT-1997.  
 19-MAR-1997; 97WO-GB00746.  
 22-MAR-1996; 96GB-0006126.  
 (BRBI-) BRITISH BIOTECH PHARM LTD.  
 Edwards RM;  
 WPI: 1997-489648/45.  
 N-PSDB; AAT85308.  
 Cells for surface expression of mutants of natural G-protein  
 receptor - where the mutants can bind a ligand that the natural  
 receptor cannot, useful as biosensors  
 Example 1; Pages 13-15; 35pp; English.  
 The present sequence is the Saccharomyces cerevisiae alpha  
 mating factor receptor Ste2, which was used in the development of  
 a method to prepare cells presenting on their surface a mutant  
 G-protein coupled receptor (GPCR) binding a desired ligand which  
 the natural receptor cannot. The method comprises generating  
 replicable expression plasmids comprising a coding sequence for a  
 GPCR mutated by one or more amino acids in its transmembrane and/or  
 extracellular domains, and operatively linked expression control  
 sequences, transforming host cells with the plasmids and contacting  
 the cells with the ligand and isolating those which bind. GPCR are  
 natural receptor proteins, i.e. membrane proteins that allow cells  
 to detect molecules in the extracellular environment. Cells  
 presenting mutant GPCR on their surfaces are useful as biosensors,  
 with potential applications in diagnostics and environmental and  
 on-line process monitoring.  
 Sequence 481 AA;  
 Query Match 83.8%; Score 67; DB 18; Length 481;  
 Best Local Similarity 92.3%; Pred. No. 0.012;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 YPVDVDPYAGSGS 13  
 Db 447 ypydvpdyagsts 459  
 RESULT 6  
 AAB03963  
 ID AAB03963 standard; Peptide: 16 AA.  
 XX AC AAB03963;  
 XX XX 26-FEB-2001 (first entry)  
 DT  
 XX pTAT-HA linker polypeptide.  
 DE Chimeric protein; fusion protein; FLICE like inhibitor protein;  
 KW FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;  
 KW tumour specific antigen; immune response; therapy; prophylaxis;  
 KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;  
 KW acquired immune deficiency syndrome.  
 XX Human immunodeficiency virus.  
 OS  
 XX WO200059935-A1.  
 PN  
 XX

PD 12-OCT-2000.  
 XX 05-APR-2000; 2000WO-US09002.  
 XX 05-APR-1999; 99US-0127867.  
 PR 06-APR-1999; 99US-0128021.  
 XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
 PA (PAYA/) PAYA C.  
 PA (ALGE/) ALGECIRAS-SCHMINICH A.  
 XX  
 XX Paya C, Algeciras-schminich A;  
 XX WPI; 2000-664988/64.  
 DR N-PSDB; AAA54300.  
 XX  
 PT Fusion polypeptide useful for inhibiting ligand-induced apoptosis,  
 PT comprises portion of anti-apoptotic polypeptide linked to a transport  
 PT group  
 XX  
 PS Disclosure; Fig 9; 89pp; English.  
 XX  
 CC A chimeric group or fusion peptide which comprises a portion of an  
 CC anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in  
 CC combination with a transport group is described. The transport group  
 CC is capable of transporting the chimeric group or fusion peptide  
 CC across the cell membrane. The anti-apoptotic polypeptide is FLICE-like  
 CC inhibitor protein (FLIP) which inhibits Fas and TNF mediated apoptosis  
 CC by inhibiting binding of Caspase-8 to the Fas receptor complex, thus  
 CC shutting off the downstream Fas signalling pathway. The chimeric group  
 CC and fusion peptide are useful for inhibiting ligand-induced apoptosis  
 CC by bringing them into contact with T cells. The chimeric group is  
 CC useful for expanding T cells in vitro e.g. T cells specific for  
 CC particular antigens such as tumour-specific antigen, for enhancing  
 CC immune response and to inhibit the apoptosis of chronically activated  
 CC T cells e.g. activated CD4<sup>+</sup> T cells in HIV infected patients. The  
 CC chimeric group is also useful for therapeutic, prophylactic or  
 CC diagnosis of intracellular delivery of small molecules and  
 CC macromolecules such as anti-apoptotic polypeptides and nucleic  
 CC acids encoding such polypeptides. Two primers (AAA54297, AAA54298) were  
 CC used to amplify the FLIP cDNA for subcloning into the XhoI-NcoI  
 CC site of the pHA-TAT vector which contains the N-terminal protein  
 CC transduction domain from the human immunodeficiency virus tat  
 CC protein. Tat is a preferred transport moiety.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 81.2%; Score 65; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.00071;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YPYDVPDYAGS 11  
 Db | | | | | | | | | |  
 4 YPYDVPDYAGS 14  
 RESULT 7  
 AAB29443  
 ID AAB29443 standard; peptide; 16 AA.  
 AC AAB29443;  
 XX  
 XX 09-FEB-2001 (first entry)  
 XX pTAT-HA linker-encoded peptide.  
 XX  
 KW Protein transduction domain; fusion molecule; therapeutic agent;  
 KW drug targeting; drug discovery; cell transduction; bioavailability;  
 KW vaccine; nervous system disorder; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy;  
 KW seizure; compulsive behaviour; meningitis; encephalitis; ischaemia;  
 KW spongiform encephalopathy; dyslexia; age-related memory loss;

KW Lou Gehring's disease; viral infection; HIV; bacterial infection.  
 XX Human immunodeficiency virus.  
 OS Synthetic.  
 XX WO200062067-A1.  
 PN 19-OCT-2000.  
 XX 28-FEB-2000; 2000WO-US05097.  
 PF 28-FEB-1999; 99US-0122757.  
 PR 29-AUG-1999; 99US-0151291.  
 XX (UNIW ) UNIV WASHINGTON.  
 PA Dowdy SF;  
 XX WPI; 2000-647439/62.  
 FI N-PSDB; AAC63859.  
 DR  
 DR Fusion molecules comprising protein transduction domains and  
 XX therapeutic agents, useful for treating e.g. Alzheimer's and  
 XX Parkinson's diseases, dementia and epilepsy -  
 PT Example 1; Fig 2; 191pp; English.  
 PT  
 PS The invention relates to a novel fusion molecule comprising at least  
 XX one protein transduction domain (PTD) and at least one linked molecule,  
 CC where the linked molecule has therapeutic or prophylactic activity  
 CC against a medical condition. The invention also relates to methods of  
 CC drug discovery in which the test compound is linked to a suitable  
 CC transducing protein and introduced to a cell; a method of killing  
 CC resistant microorganisms using a suitable fusion molecule; a mammal  
 CC comprising a covalently linked fusion molecule; and a mammal adapted for  
 CC experimental use in which at least one transduction molecule has been  
 CC transduced into essentially all the cells of the mammal. The fusion  
 CC molecule is used to deliver a therapeutic agent to a mammal, especially  
 CC a human. The linked molecule may be a vaccine, an anti-infective drug,  
 CC a cardiovascular drug, an antitumour drug, an analgesic, an  
 CC antiinflammatory, a diagnostic marker or a drug for the treatment or  
 CC prevention of a central or peripheral nervous system disorder. The  
 CC central nervous system (CNS) disorder is especially Alzheimer's disease,  
 CC Parkinson's disease, Huntington's disease, and also includes pre-senile  
 CC dementia, epilepsy and seizures, compulsive behaviour, meningitis  
 CC (including viral and bacterial meningitis), encephalitis, ischaemia,  
 CC scrapie (or related spongiform encephalopathies), dyslexia, age-related  
 CC memory loss or Lou Gehring's disease. Fusion molecules can also be  
 CC used to kill virally infected cells, especially those infected with HIV.  
 CC The vaccines are used to treat or prevent bacterial or viral infections.  
 CC The methods are a highly effective means for transducing a molecule  
 CC into an entire mammal or into specific cells, tissues, organs and  
 CC systems within it. They also overcome bioavailability problems that  
 CC are associated with many therapeutic agents (e.g., large molecular size,  
 CC hydrophobicity, hydrophilicity, biological resistance), by providing  
 CC efficient transduction of the target cell. The present sequence  
 CC represents a protein transduction domain used in the invention.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 81.2%; Score 65; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.00071;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YPYDVPDYAGS 11  
 Db | | | | | | | | | |  
 4 YPYDVPDYAGS 14  
 RESULT 8  
 AAW41032  
 ID AAW41032 standard; Protein; 17 AA.

XX AAW41032;  
 AC  
 XX  
 DT  
 XX  
 XX  
 DE  
 XX  
 XX  
 KW Transdominant bioactive agent; phenotype alteration; signalling pathway;  
 KW antitumour agent; cardiovascular disease; angiogenesis; atherosclerosis;  
 KW obesity; neurodegeneration; bone disease; infection; allergy; therapy;  
 KW flu-epitope peptide.  
 XX  
 OS Synthetic.  
 OS Influenza virus.  
 XX  
 XX WO9727213-A1.  
 PN  
 XX  
 XX 31-JUL-1997.  
 PD  
 XX  
 XX 23-JAN-1997; 97WO-US01048.  
 PF  
 XX  
 XX 23-JAN-1996; 96US-0589911.  
 PR  
 XX 23-JAN-1996; 96US-0589109.  
 PR  
 XX  
 XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA  
 XX  
 XX Noaln GP, Rothenberg SM;  
 PI  
 XX  
 XX WPI; 1997-393612/36.  
 DR  
 XX  
 XX Screening for trans-dominant active agents able to alter cell  
 PT phenotype - useful to identify potential drugs with e. g.  
 PT anti-tumour activity  
 PT  
 XX  
 XX Example 1; Page 53; 91pp; English.  
 PS  
 XX  
 CC This sequence represents a scrambled flu-epitope peptide, and can be  
 CC used in the method of the invention. The method is for screening for  
 CC transdominant bioactive agents (A) able to alter the phenotype of a cell  
 CC comprises: (a) introducing a library of different randomised nucleic  
 CC acids (1) into cells; and (b) screening the cells for altered phenotype  
 CC due to presence of (A). (A) are potential pharmaceuticals, from their  
 CC effect on signalling pathways. A particular application is to identify  
 CC peptides, encoded by (1), that have antitumour activity or are able to  
 CC increase sensitivity to, or reduce toxicity of, known antitumour agents.  
 CC More generally the method can identify agents for treatment of many other  
 CC conditions, e.g. cardiovascular diseases, angiogenesis, atherosclerosis,  
 CC obesity, neurodegeneration, bone disease, viral and other infections,  
 CC allergy etc.  
 CC  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 81.2%; Score 65; DB 18; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.00076;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YPYDVPDYAGS 11  
 Db 5 ypydvpdyags 15  
 RESULT 9  
 AAW29116  
 ID AAW29116 standard; Peptide; 17 AA.  
 XX  
 AC AAW29116;  
 XX  
 XX 04-FEB-1998 (first entry)  
 DT  
 XX  
 XX Flu epitope tagged scrambled peptide.  
 DE  
 XX Transdominant intracellular effector peptide; RNA; screening;  
 KW

KW altered phenotype; retrovirus; library; signal transduction;  
 KW antitumour; PBABE; influenza virus; flu; epitope.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9727212-A1.  
 XX  
 XX 31-JUL-1997.  
 PD  
 XX  
 XX 23-JAN-1997; 97WO-US01019.  
 PF  
 XX  
 XX 23-JAN-1996; 96US-0589911.  
 PR  
 XX 23-JAN-1996; 96US-0589109.  
 PR  
 XX  
 XX (RIGE-) RIGEL PHARM INC.  
 PA  
 XX  
 XX Noaln GP;  
 PI  
 XX  
 XX WPI; 1997-393611/36.  
 DR  
 XX  
 XX Screening for transdominant intracellular active agents able to  
 PT alter cell phenotype - useful for examining for changed phenotype,  
 PT particularly to identify potential drugs with e. g. antitumour  
 PT activity  
 PT  
 XX  
 XX Example 1; Page 53; 91pp; English.  
 PS  
 XX  
 CC This peptide comprises a Flu epitope tagged scrambled peptide.  
 CC Murine 10T1/2 Clone 8 cells were infected with phabe puro  
 CC retrovirus constructs containing a sequence coding for the Flu  
 CC scrambled epitope or an inhibitor peptide (see AAW29117) identical  
 CC to the C2 region of protein kinase C (PKA) isozymes. Control clone  
 CC 8 cells showed predominantly cytoplasmic and perinuclear staining,  
 CC while PMA induced cells showed translocation to the nucleus. Cells  
 CC infected with constructs coding for the scrambled peptide showed  
 CC similar staining. Those infected with constructs coding for  
 CC the C2 region showed predominantly cytoplasmic and perinuclear  
 CC staining in both control and PMA induced cells. Novel outcomes can  
 CC occur upon expression of peptides in cells. A claimed method of  
 CC screening for transdominant intracellular bioactive agents (A) able  
 CC to alter the phenotype of a cell comprises: (a) introducing a  
 CC library of different randomised nucleic acids (1) into cells; and  
 CC (b) screening the cells for altered phenotype due to presence of  
 CC (A). Also new are: (1) a library of retroviruses containing  
 CC different randomised (1); and (2) a library of mammalian cells  
 CC containing the library of (1), preferably integrated into the  
 CC genome.  
 CC  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 81.2%; Score 65; DB 18; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.00076;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YPYDVPDYAGS 11  
 Db 5 ypydvpdyags 15  
 RESULT 10  
 AAB45969  
 ID AAB45969 standard; Peptide; 17 AA.  
 XX  
 AC AAB45969;  
 XX  
 XX 02-APR-2001 (first entry)  
 DT  
 XX  
 XX Transdominant effector peptide associated screening peptide #49.  
 DE  
 XX Intracellular transdominant bioactive agent; screening; cell phenotype;  
 KW effector peptide.  
 KW  
 XX

OS Unidentified.  
XX US6153380-A.  
PN  
XX  
PD 28-NOV-2000.  
XX  
XX 23-JAN-1997; 97US-0789333.  
PF  
XX 23-JAN-1996; 96US-0589108.  
PR  
XX 23-JAN-1996; 96US-0589911.  
PR  
XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (RIGE-) RIGEL PHARM INC.  
XX  
XX Rothenberg SM, Nolan GP;  
PI  
XX  
XX WPI; 2001-060084/07.  
DR  
XX  
XX Methods for screening intracellular transdominant effector peptides and  
PT RNA molecules comprise delivering random oligonucleotides to cells,  
PT which are then screened for an altered phenotype .  
XX  
XX Example 1; Column 79-80; 57pp; English.  
PS  
XX  
XX This invention describes novel in vitro screening methods (I) for a  
CC transdominant intracellular bioactive agent capable of altering the  
CC phenotype of a cell. (I) comprises: (a) introducing a molecular library  
CC of randomized candidate nucleic acids into several cells; and (b)  
CC screening the cells for a cell exhibiting an altered phenotype, where the  
CC altered phenotype is due to the presence of a transdominant bioactive  
CC agent. The methods are particularly useful for screening intracellular  
CC transdominant effector peptides and RNA molecules selected inside living  
CC cells from randomized pools. (I) is also useful for introducing random  
CC libraries into cells to screen for bioactive compounds. The methods allow  
CC rapid and highly efficient screening of large numbers of random  
CC oligonucleotides and their corresponding expression products in a single  
CC step. In addition, the methods allow screening in the absence of  
CC significant prior characterization of the cellular defect.  
XX  
XX Sequence 17 AA;  
SQ

Query Match 81.2%; Score 65; DB 22; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.00076;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGS 11  
| | | | | | | | | |  
Db 5 YPYDVPDYAGS 15

RESULT 11  
AAW48631  
ID AAW48631 standard; peptide; 25 AA.  
XX  
XX AAW48631;  
AC  
XX 11-SEP-1998 (first entry)  
DT  
XX Chimeric adenoviral penton base protein epitope 3.  
XX  
XX Short-shafted adenoviral fibre; ssAF; penton base; cystic fibrosis;  
KW binding site; binding domain; cell surface binding site; gene therapy;  
KW bispecific antibody; HIV; cancer.  
XX  
XX Unidentified.  
OS  
XX WO9807877-A1.  
PN  
XX  
XX 26-FEB-1998.  
PD  
XX  
XX 21-AUG-1997; 97WO-US14718.  
PF  
XX  
XX 21-AUG-1996; 96US-0700846.  
PR

XX (GENV-) GENVEC INC.  
PA  
XX Kovesdi I, Roelvink PW, Wickham TJ;  
PI  
XX WPI; 1998-169180/15.  
DR  
XX Short-shafted adenoviral fibre constructs - used for producing  
PT products that facilitate entry into target cells, useful for gene  
PT therapy of cellular disorders  
PF  
XX  
XX PS Disclosure; Page 39; 98pp; English.  
XX  
XX The present peptide sequence is incorporated into an adenoviral fiber.  
CC The fiber protein and its penton base are used by the adenovirus to  
CC interact with distinct cellular receptors to attach to and efficiently  
CC infect a cell. The invention claims for a transfer vector which contains  
CC DNA encoding a short-shafted adenoviral fibre (ssAF). The adenoviral  
CC penton base can be modified by incorporating sequences for a ligand to a  
CC cell surface receptor or sequences that allow binding to a bispecific  
CC antibody. Bispecific antibodies raised against the present peptide  
CC allows one end of the antibody molecule to bind to the fiber and the  
CC other end to bind specifically to a cell surface receptor. Therefore  
CC this method enables targeting of the adenovirus to a desired cell-surface  
CC receptor by the introduction of a non-native amino acid sequence either  
CC into the penton base or the fibre knob. The non-native amino acid  
CC sequence can be such that it enables direct or indirect binding, e.g. by  
CC means of a bispecific or multispecific binding agent, of the adenovirus  
CC to the desired cell-surface receptor. Using the a short shafted  
CC adenovirus to attach to a cell and therefore effect entry into the cell  
CC would reduce the level or efficiency of adenoviral fibre binding to its  
CC cell-surface receptor and increase the adenoviral penton base binding to  
CC its cell-surface receptor, thereby increasing the specificity of binding  
CC of the adenovirus to a given cell. The transfer vector is claimed  
CC to be useful for expressing therapeutic genes, for treating inherited  
CC diseases such as cystic fibrosis or for inducing cell death in  
CC pathogenic infections (e.g. HIV infections) and cancers.  
XX  
XX Sequence 25 AA;  
SQ

Query Match 81.2%; Score 65; DB 19; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGS 11  
| | | | | | | | | |  
Db 14 YPYDVPDYAGS 24

RESULT 12  
AAW46332  
ID AAW46332 standard; Peptide; 25 AA.  
XX  
XX AAW46332;  
AC  
XX 08-MAY-1998 (first entry)  
DT  
XX Haemagglutinin sequence of a chimeric adenovirus penton base protein.  
XX  
XX Integrin; cell surface receptor; penton base protein; adenovirus;  
KW binding site; binding domain; cell surface binding site; gene therapy;  
KW bispecific molecule; adenoviral transfer vector; pAT.  
XX  
XX Synthetic.  
OS  
XX US5712136-A.  
PN  
XX 27-JAN-1998.  
PD  
XX 17-APR-1996; 96US-0634060.  
PF  
XX  
XX 08-SEP-1994; 94US-0303162.  
PR

XX (GENV-) GENVEC INC.  
 XX Brough DE, Bruder JT, Kovessi I, McVey DL, Roelvink PW;  
 PI Wickham TJ;  
 XX  
 XX WPI; 1998-119984/11.  
 DR N-PSDB; AAV04953-54.  
 XX  
 XX Methods for introducing adenovirus into cells - used for genetic  
 PT engineering and gene therapy  
 XX  
 XX Example 13; Column 34; 56pp; English.  
 PS  
 XX The present sequence represents a haemagglutinin sequence of a chimeric  
 CC adenovirus penton base protein. The peptide is encoded by overlapping  
 CC oligonucleotides. The penton base protein binds to cell surface receptors  
 CC called integrins. The integrins not only provide a binding site for the  
 CC adenoviral penton base protein, but also mediate cellular adhesion to  
 CC the extracellular matrix molecules. The specification describes a method  
 CC of introducing an adenovirus into a cell in vitro having a particular  
 CC cell surface binding site. The adenovirus is contacted with a bispecific  
 CC molecule comprising a component that selectively binds a binding domain  
 CC of the penton base protein of the adenovirus and a second component that  
 CC selectively binds the cell surface binding site. A complex of the  
 CC adenovirus and the bispecific molecule is formed, and the cell is  
 CC contacted with it to allow entry of the adenovirus into the cell. The  
 CC methods can be used for research and the vectors can be used for gene  
 CC therapy.  
 XX  
 XX Sequence 25 AA;  
 SQ  
 Query Match 81.2%; Score 65; DB 19; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YPYDVPDYAGS 11  
 Db 14 ypydvpdyags 24  
 RESULT 13  
 AAR81452  
 ID AAR81452 standard; Peptide; 15 AA.  
 XX  
 AC AAR81452;  
 XX  
 DT 02-JUL-1996 (first entry)  
 XX  
 DE Haemagglutinin tag peptide.  
 XX  
 KW Bcl-Y; apoptosis; cell proliferation; cell death; diagnosis;  
 KW gene therapy; haemagglutinin; HA tag.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9605232-A1.  
 XX  
 PD 22-FEB-1996.  
 XX  
 PF 09-AUG-1995; 95WO-US10103.  
 XX  
 PR 11-OCT-1994; 94US-0321071.  
 PR 09-AUG-1994; 94US-0287427.  
 XX  
 PA (IMMU-) IMMUNOGEN INC.  
 XX  
 PI Chittenden TD;  
 XX  
 XX WPI; 1996-139648/14.  
 DR  
 XX  
 PT New Isolated human Bcl-Y protein - used to develop prods. for

PT treating disorders characterised by inappropriate cell proliferation  
 PT or cell death  
 XX  
 XX Example 1; Page 65; 100pp; English.  
 PS  
 XX A haemagglutinin (HA) tag peptide (AAR81452) was expressed as a  
 CC fusion with amino acids 2-221 of apoptosis-associated protein  
 CC Bcl-Y (see AAR81451) following PCR amplification (see AAT17378-79)  
 CC of Bcl-Y cDNA and insertion into a CMV-based pcDNA1/amp  
 CC vector derivative. The HA-Bcl-Y protein was produced in vitro  
 CC and in transfected COS7 and NIH3T3 cells.  
 XX  
 XX Sequence 15 AA;  
 SQ  
 Query Match 78.8%; Score 63; DB 17; Length 15;  
 Best Local Similarity 84.6%; Pred. No. 0.0014;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 YPYDVPDYAGSGS 13  
 Db 3 ypydvpdyags 15  
 RESULT 14  
 AAB10433  
 ID AAB10433 standard; Protein; 228 AA.  
 XX  
 AC AAB10433;  
 XX  
 DT 01-DEC-2000 (first entry)  
 XX  
 DE Expression vector pSEX11G2 protein G.  
 XX  
 KW Expression vector; antibody binding protein; monoclonal antibody; Neo-R;  
 KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.  
 XX  
 OS Synthetic.  
 XX  
 PN DE19900635-A1.  
 XX  
 PD 13-JUL-2000.  
 XX  
 PF 11-JAN-1999; 99DE-1000635.  
 XX  
 PR 11-JAN-1999; 99DE-1000635.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Breittling F, Poustka A, Moldenhauer G;  
 XX  
 DR WPI; 2000-499832/45.  
 DR N-PSDB; AAA71429.  
 XX  
 PT Selecting monoclonal antibodies, by expressing them on the surface of  
 PT hybridomas attached to antibody-binding protein, then reaction with  
 PT antibody library -  
 XX  
 PS Claim 16; Fig 2; 22pp; German.  
 XX  
 CC This invention describes a novel method for the selection of monoclonal  
 CC antibodies (MAB) which comprises (i) fusing B lymphocytes with myeloma  
 CC cells to produce antibody-producing hybridomas such that the antibodies  
 CC are presented at the surface of the hybridomas by an antibody-binding  
 CC protein (I); and (ii) binding the antibody to antigens (Ag). The  
 CC invention also describes antibody-binding proteins (I) that comprise a  
 CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa  
 CC chain or a murine MHC (major histocompatibility complex) class I k(k)  
 CC molecule; an antibody-binding site of proteins A, G, L or LG, and the  
 CC transmembrane domain of pDcFR (platelet-derived growth factor receptor)  
 CC or CD52. The method is used to select MAB with specificity for particular  
 CC antigens. MAB can be selected without separate culture of hybridomas,  
 CC and selection can be made against many antigens in a library, optionally

CC on the basis of strength of affinity for a particular antigen. Complex  
CC mixtures of hybridomas can be used for selection, reducing the time and  
CC cost involved in MAB selection. This sequence represents the protein G  
CC contained in the expression vector pSEX11G2 which contains the protein G,  
CC Neo-R and the bla protein described in the method of the invention.  
XX  
SQ Sequence 228 AA;

Query Match 77.5%; Score 62; DB 21; Length 228;  
Best Local Similarity 90.9%; Pred. No. 0.034;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGS 11  
| | | | | | | | | |  
Db 22 YPYDVPDYAGA 32

RESULT 15  
AAY00874  
ID AAY00874 standard; Protein: 232 AA.  
XX  
AC AAY00874;  
XX  
DT 21-MAY-1999 (first entry)  
XX  
DE PHOOK-1.GM-CSF fusion protein sequence.  
XX  
KW GM-CSF; granulocyte macrophage colony stimulating factor; vaccine;  
KW membrane-bound fusion protein; non-antibody immunomodulator; infection;  
KW membrane attachment domain; cancer; autoimmune disease; therapy.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 220 /note= "unspecified amino acid"  
ET  
XX WO9906544-A1.  
PN 11-FEB-1999.  
XX  
PD 28-JUL-1998; 98WO-US15622.  
XX  
PF 29-JUL-1997; 97US-0902516.  
XX  
PR (IMMU-) IMMUNE RESPONSE CORP.  
XX  
PA  
XX  
XX Soo Hoo W;  
PI  
XX  
XX WPI; 1999-153774/13.  
DR N-PSDB; AAX27068.  
XX  
XX Vaccine having a membrane-bound fusion protein - comprising an  
PT immunomodulator and heterologous membrane attachment domain useful  
PT for modulation of immune response against a disease-associated  
PT antigen  
XX  
XX Example 1; Fig 2a-b; 91pp; English.

CC This sequence is the PHOOK-1.GM-CSF fusion protein. The  
CC invention relates to a vaccine comprising a cell having a membrane-bound  
CC fusion protein (FP) consisting of a non-antibody immunomodulator (I)  
CC linked to a heterologous membrane attachment domain. The vaccines are  
CC used to treat or prevent a wide variety of cancers (e.g. of colon, breast  
CC or prostate, melanoma, glioma), alone or as adjunct to other therapies;  
CC autoimmune diseases (e.g. rheumatoid arthritis, psoriasis, multiple  
CC sclerosis, systemic lupus erythematosus, type I diabetes, allergy)  
CC or viral, bacterial or parasitic infections (e.g. human immune  
CC deficiency virus, Helicobacter pylori, Porphyromonas gingivalis, or  
CC Candida albicans). A panel of cells (or cell lines) each genetically  
CC modified to express different antigens can be maintained as a repository,

CC for treatment or prevention of the appropriate tumour type, e.g. based on  
CC histological analysis. Membrane-bound (I) provides a vaccine with  
CC increased receptor-cytokine avidity, and thus stimulates a stronger  
CC immune response.  
XX  
SQ Sequence 232 AA;

Query Match 77.5%; Score 62; DB 20; Length 232;  
Best Local Similarity 90.9%; Pred. No. 0.035;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGS 11  
| | | | | | | | | |  
Db 22 YPYDVPDYAGA 32

Search completed: April 11, 2002, 10:15:43  
Job time: 93 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 11, 2002, 10:14:43 ; Search time 24.73 Seconds  
(without alignments)  
12.739 Million cell updates/sec

Title: US-09-284-787-2

Perfect score: 80

Sequence: 1 YPYDVPDYAGSGSK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	81.2	16	4	US-09-208-966-15
2	65	81.2	17	4	US-08-789-333F-51
3	65	81.2	25	1	US-08-634-060-27
4	65	81.2	25	2	US-08-700-846-10
5	63	78.8	15	1	US-08-321-071A-5
6	62	77.5	219	2	US-08-902-516-2
7	61	76.2	10	3	US-08-990-140-13
8	60.5	75.6	102	1	US-08-282-951-2
9	60.5	75.6	272	1	US-08-282-951-6
10	59	73.8	14	2	US-08-723-726-1
11	59	73.8	16	3	US-08-390-874C-13
12	59	73.8	16	4	US-09-365-772-13
13	59	73.8	19	4	US-09-169-015-52
14	59	73.8	27	4	US-08-672-213-39
15	59	73.8	40	4	US-08-672-213-29
16	59	73.8	389	2	US-08-802-322-14
17	57	71.2	13	1	US-08-660-626-11
18	57	71.2	13	4	US-09-031-168-11
19	55.5	69.4	32	2	US-09-066-074-7
20	55.5	69.4	32	2	US-08-555-912A-7
21	55	68.8	9	1	US-08-011-398B-6
22	55	68.8	9	1	US-08-090-148-2
23	55	68.8	9	1	US-08-370-225-6
24	55	68.8	9	1	US-08-167-982-1
25	55	68.8	9	1	US-08-634-060-31
26	55	68.8	9	1	US-08-464-051-6
27	55	68.8	9	1	US-08-461-859-6

28	55	68.8	9	1	US-08-470-837-28	Sequence 28, Appl
29	55	68.8	9	2	US-08-478-386A-19	Sequence 19, Appl
30	55	68.8	9	2	US-08-292-597-19	Sequence 19, Appl
31	55	68.8	9	2	US-08-462-498-6	Sequence 6, Appl
32	55	68.8	9	2	US-08-922-267A-60	Sequence 60, Appl
33	55	68.8	9	2	US-08-388-653-19	Sequence 19, Appl
34	55	68.8	9	2	US-08-473-985-19	Sequence 19, Appl
35	55	68.8	9	2	US-08-690-011A-17	Sequence 17, Appl
36	55	68.8	9	2	US-08-690-011A-49	Sequence 49, Appl
37	55	68.8	9	2	US-08-685-625A-4	Sequence 4, Appl
38	55	68.8	9	2	US-08-687-559-14	Sequence 14, Appl
39	55	68.8	9	2	US-08-700-846-11	Sequence 11, Appl
40	55	68.8	9	2	US-08-287-537B-3	Sequence 3, Appl
41	55	68.8	9	2	US-08-483-898-19	Sequence 19, Appl
42	55	68.8	9	3	US-09-087-716-19	Sequence 19, Appl
43	55	68.8	9	3	US-08-853-733B-28	Sequence 28, Appl
44	55	68.8	9	3	US-08-554-385-6	Sequence 6, Appl
45	55	68.8	9	3	US-09-157-753-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-208-966-15

; Sequence 15, Application US/09208966

; Patent No. 6221355

; GENERAL INFORMATION:

; APPLICANT: Dowdy, Steven F.

; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF

; FILE REFERENCE: 48881/1742

; CURRENT APPLICATION NUMBER: US/09/208,966

; CURRENT FILING DATE: 1998-12-10

; EARLIER APPLICATION NUMBER: 60/082,402

; EARLIER FILING DATE: 1998-04-20

; EARLIER APPLICATION NUMBER: 60/069,012

; EARLIER FILING DATE: 1997-12-10

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15

; LENGTH: 16

; TYPE: PRT

; ORGANISM: human

; US-09-208-966-15

Query Match 81.2% Score 65; DB 4; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00034;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGS 11

Db 4 YPYDVPDYAGS 14

RESULT 2

US-08-789-333F-51

; Sequence 51, Application US/08789333F

; Patent No. 6153380

; GENERAL INFORMATION:

; APPLICANT: No. 6153380an, Garry P

; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR

; TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES

; FILE REFERENCE: A643601DJBRMSDSS

; CURRENT APPLICATION NUMBER: US/08/789,333F

; CURRENT FILING DATE: 1997-01-23

; PRIOR APPLICATION NUMBER: 08/589,108

; PRIOR FILING DATE: 1996-01-23

; PRIOR APPLICATION NUMBER: 08/589,911

; PRIOR FILING DATE: 1996-01-23

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 51  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: epitope tag  
OTHER INFORMATION: sequence.  
US-08-789-333F-51

Query Match 81.2%; Score 65; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.00037;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGS 11  
|||||

DB 5 YPYDVPDYAGS 15  
|||||

RESULT 3  
US-08-634-060-27  
Sequence 27, Application US/08634060  
Patent No. 5712136  
GENERAL INFORMATION:  
APPLICANT: Wickham, Thomas J.  
APPLICANT: Kovesdi, Imre  
APPLICANT: Roelvink, Petrus W.  
TITLE OF INVENTION: ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY  
TITLE OF INVENTION: THE ADENOVIRUS PENTON BASE PROTEIN  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Volt & Mayer, Ltd.  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,060  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/303,162  
FILING DATE: 08-SEP-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kilyk, John Jr.  
REGISTRATION NUMBER: 30763  
REFERENCE/DOCKET NUMBER: 71602  
TELEPHONE: (312) 616-5600  
TELEFAX: (312) 616-5700  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-634-060-27

Query Match 81.2%; Score 65; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.00055;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGS 11  
|||||

DB 14 YPYDVPDYAGS 24

RESULT 4  
US-08-700-846-10  
Sequence 10, Application US/08700846  
Patent No. 5962311  
GENERAL INFORMATION:  
APPLICANT: WICKHAM, THOMAS J.  
APPLICANT: ROELVINK, PETRUS W.  
APPLICANT: KOVESDI, IMRE  
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS  
TITLE OF INVENTION: USE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.  
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900  
CITY: CHICAGO  
STATE: IL  
COUNTRY: USA  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,846  
FILING DATE: 21-AUG-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: LARCHER, CAROL  
REGISTRATION NUMBER: 35243  
REFERENCE/DOCKET NUMBER: 74294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 616-5600  
TELEFAX: (312) 616-5700  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-700-846-10

Query Match 81.2%; Score 65; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.00055;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGS 11  
|||||

DB 14 YPYDVPDYAGS 24

RESULT 5  
US-08-321-071A-5  
Sequence 5, Application US/08321071A  
Patent No. 5672686  
GENERAL INFORMATION:  
APPLICANT: CHITTENDEN, Thomas D.  
TITLE OF INVENTION: APOPTOSIS RELATED PROTEIN Bcl-Y, AND METHODS  
TITLE OF INVENTION: OF USE THEREOF  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/321,071A  
FILING DATE: 11-OCT-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10103  
FILING DATE: 09-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/287,427  
FILING DATE: 09-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, HENRY N.  
REGISTRATION NUMBER: 32,073  
REFERENCE/DOCKET NUMBER: 104322.121CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-942-8400  
TELEFAX: 202-942-8484  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-321-071A-5

Query Match 78.8%; Score 63; DB 1; Length 15;  
Best Local Similarity 84.8%; Pred. No. 0.00066;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGSGS 13  
|||||  
Db 3 YPYDVPDYASLGS 15

RESULT 6  
US-08-902-516-2  
; Sequence 2, Application US/08902516  
; Patent No. 5891432  
; GENERAL INFORMATION:  
; APPLICANT: SOO HOO, William  
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
; TITLE OF INVENTION: RESPONSE USING SAME  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL & FLORES, LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,516  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-IM 2442  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)535-9001  
; TELEFAX: (619)535-8949  
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-902-516-2  
Query Match 77.5%; Score 62; DB 2; Length 219;  
Best Local Similarity 90.9%; Pred. No. 0.016;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YPYDVPDYAGS 11  
|||||  
Db 22 YPYDVPDYAGA 32  
RESULT 7  
US-08-990-140-13  
; Sequence 13, Application US/08990140A  
; Patent No. 6093795  
; GENERAL INFORMATION:  
; APPLICANT: Olsen, Henrik S.  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Sonenberg, Nahum  
; APPLICANT: Methot, Nathalie  
; APPLICANT: Rom, Eran  
; TITLE OF INVENTION: Human P71-like Subunit Protein (hP71) and Human  
; TITLE OF INVENTION: eIF4G-like Protein (p97) Genes  
; FILE REFERENCE: 1488 0700001  
; CURRENT APPLICATION NUMBER: US/08/990,140A  
; CURRENT FILING DATE: 1997-12-12  
; EARLIER APPLICATION NUMBER: US 60/033,151  
; EARLIER FILING DATE: 1996-12-13  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-990-140-13

Query Match 76.2%; Score 61; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00088;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYAG 10  
|||||  
Db 1 YPYDVPDYAG 10

RESULT 8  
US-08-282-951-2  
; Sequence 2, Application US/08282951  
; Patent No. 5665590  
; GENERAL INFORMATION:  
; APPLICANT: YANG, ZHI  
; TITLE OF INVENTION: METHOD FOR ISOLATING AND DIRECTLY  
; TITLE OF INVENTION: CLONING GENES WHICH ENCODE CELL-SURFACE AND SECRETED  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,951  
FILING DATE: 29-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 20296-20012.00  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 102 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-282-951-2

Query Match 75.6%; Score 60.5; DB 1; Length 102;  
Best Local Similarity 75.0%; Pred. No. 0.012;  
Matches 12; Conservative 1; Mismatches 0; Indels 3; Gaps 1;  
Qy 1 YPYDVPDYA---GSGS 13  
Db 56 YPYDVPDYAPNKGSGT 71

RESULT 9  
US-08-282-951-6  
Sequence 6, Application US/08282951  
Patent No. 5665590  
GENERAL INFORMATION:  
APPLICANT: YANG, ZHI  
TITLE OF INVENTION: METHOD FOR ISOLATING AND DIRECTLY  
CLONING GENES WHICH ENCODE CELL-SURFACE AND SECRETED  
PROTEINS  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,951  
FILING DATE: 29-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 20296-20012.00  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 272 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-282-951-6

Query Match 75.6%; Score 60.5; DB 1; Length 272;  
Best Local Similarity 75.0%; Pred. No. 0.035;  
Matches 12; Conservative 1; Mismatches 0; Indels 3; Gaps 1;  
Qy 1 YPYDVPDYA---GSGS 13  
Db 227 YPYDVPDYAPNKGSGT 242  
RESULT 10  
US-08-723-726-1  
Sequence 1, Application US/08723726  
Patent No. 5851521  
GENERAL INFORMATION:  
APPLICANT: BRANELLEC, Didier  
APPLICANT: WALSH, Kenneth  
APPLICANT: ISNER, Jeffrey M.  
APPLICANT: DENEFFLE, Patrice  
TITLE OF INVENTION: VIRAL VECTORS AND THEIR USE FOR TREATING  
HYPERPROLIFERATIVE DISORDERS, IN PARTICULAR RESTENOSIS  
TITLE OF INVENTION: HYPERPROLIFERATIVE DISORDERS, IN PARTICULAR RESTENOSIS  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: Mail Drop 3C43, P.O. Box 5093  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426-0997  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,726  
FILING DATE: 30-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US96/04493  
FILING DATE: 28-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95-04234  
FILING DATE: 31-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky, Martin F.  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: ST95022A-US  
TELEPHONE: (610)454-3816  
TELEFAX: (610)454-3808  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-723-726-1

Query Match 73.8%; Score 59; DB 2; Length 14;  
Best Local Similarity 83.3%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 YPYDVPDYAGSG 12  
Db 1 YPYDVPDYASLG 12  
RESULT 11  
US-08-390-874C-13

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; Sequence 13, Application US/08390874C
; Patent No. 6043062
; GENERAL INFORMATION:
; APPLICANT: Klippel, Anke
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: A Constitutively Active
; TITLE OF INVENTION: Phosphatidylinositol 3-Kinase and Uses Thereof
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,874C
; FILING DATE: 17-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 02307K-057000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-390-874C-13

Query Match 73.8%; Score 59; DB 3; Length 16;
Best Local Similarity 83.3%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSG 12
Db 2 YPYDVPDYASLG 13

RESULT 12
US-09-265-772-13
; Sequence 13, Application US/09265772
; Patent No. 6300111
; GENERAL INFORMATION:
; APPLICANT: Klippel, Anke
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: A Constitutively Active
; TITLE OF INVENTION: Phosphatidylinositol 3-Kinase and Uses Thereof
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,015
; FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-169-015-52

Query Match 73.8%; Score 59; DB 4; Length 19;
Best Local Similarity 83.3%; Pred. No. 0.0035;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSG 12
Db 5 YPYDVPDYASLG 16

RESULT 14
US-08-672-213-39
; Sequence 39, Application US/08672213
; Patent No. 6305649
; GENERAL INFORMATION:
; APPLICANT: Gilman, Michael Z.
; APPLICANT: Natesan, Sridharan
; TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
; TITLE OF INVENTION: FACTORS IN GENE THERAPY
; NUMBER OF SEQUENCES: 72

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; APPLICATION NUMBER: US/09/265,772
; FILING DATE: 10-MAR-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/390,874
; FILING DATE: 17-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 02307K-057010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-265-772-13

Query Match 73.8%; Score 59; DB 4; Length 16;
Best Local Similarity 83.3%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSG 12
Db 2 YPYDVPDYASLG 13

RESULT 13
US-09-169-015-52
; Sequence 52, Application US/09169015
; Patent No. 6180343
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides
; FILE REFERENCE: A66900/DJB/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/169,015
; CURRENT FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-169-015-52

Query Match 73.8%; Score 59; DB 4; Length 19;
Best Local Similarity 83.3%; Pred. No. 0.0035;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YPYDVPDYAGSG 12
Db 5 YPYDVPDYASLG 16

RESULT 14
US-08-672-213-39
; Sequence 39, Application US/08672213
; Patent No. 6305649
; GENERAL INFORMATION:
; APPLICANT: Gilman, Michael Z.
; APPLICANT: Natesan, Sridharan
; TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
; TITLE OF INVENTION: FACTORS IN GENE THERAPY
; NUMBER OF SEQUENCES: 72

```

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARIAD Gene Therapeutics, Inc.  
; STREET: 26 Landsdowne Street  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139-4234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,213  
; FILING DATE: 27-JUN-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,553  
; FILING DATE: 27-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/019,614  
; FILING DATE: 29-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BERSTEIN, David L.  
; REGISTRATION NUMBER: 31,235  
; REFERENCE/DOCKET NUMBER: ARIAD 346B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-494-0400  
; TELEFAX: 617-494-0208  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-672-213-39

Query Match 73.8%; Score 59; DB 4; Length 27;  
Best Local Similarity 83.3%; Pred. No. 0.0051;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGSG 12  
| | | | | | | | | |  
Db 5 YPYDVPDYASLG 16

RESULT 15  
US-08-672-213-29  
; Sequence 29, Application US/08672213  
; Patent No. 6306649  
; GENERAL INFORMATION:  
; APPLICANT: GILMAN, Michael Z.  
; APPLICANT: NATESAN, Sridaran  
; TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION  
; TITLE OF INVENTION: FACTORS IN GENE THERAPY  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARIAD Gene Therapeutics, Inc.  
; STREET: 26 Landsdowne Street  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139-4234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,213  
; FILING DATE: 27-JUN-1996  
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,553  
; FILING DATE: 27-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/019,614  
; FILING DATE: 29-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BERSTEIN, David L.  
; REGISTRATION NUMBER: 31,235  
; REFERENCE/DOCKET NUMBER: ARIAD 346B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-494-0400  
; TELEFAX: 617-494-0208  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-672-213-29

Query Match 73.8%; Score 59; DB 4; Length 40;  
Best Local Similarity 83.3%; Pred. No. 0.0078;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YPYDVPDYAGSG 12  
| | | | | | | | | |  
Db 5 YPYDVPDYASLG 16

Search completed: April 11, 2002, 10:14:44  
Job time: 34 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 11, 2002, 10:16:16 ; Search time 27.06 Seconds  
(without alignments)  
39.410 Million cell updates/sec

Title: US-09-284-787-2

Perfect score: 80  
Sequence: 1 YPYDVPDYGSGSK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	55	68.8	330	2 JQ2374	hemagglutinin - in
2	55	68.8	330	2 JQ2375	hemagglutinin - in
3	55	68.8	331	2 JQ2377	hemagglutinin - in
4	55	68.8	331	2 JQ2378	hemagglutinin - in
5	55	68.8	347	2 S52173	hemagglutinin - in
6	55	68.8	347	2 S52174	hemagglutinin - in
7	55	68.8	347	2 S52175	hemagglutinin - in
8	55	68.8	347	2 S52176	hemagglutinin - in
9	55	68.8	347	2 S52178	hemagglutinin - in
10	55	68.8	347	2 S52179	hemagglutinin - in
11	55	68.8	347	2 S52180	hemagglutinin - in
12	55	68.8	347	2 S52182	hemagglutinin - in
13	55	68.8	347	2 S52183	hemagglutinin - in
14	55	68.8	347	2 S52185	hemagglutinin - in
15	55	68.8	347	2 S52186	hemagglutinin - in
16	55	68.8	347	2 S52187	hemagglutinin - in
17	55	68.8	347	2 S52188	hemagglutinin - in
18	55	68.8	347	2 S52189	hemagglutinin - in
19	55	68.8	347	2 S52191	hemagglutinin - in
20	55	68.8	347	2 S52195	hemagglutinin - in
21	55	68.8	347	2 S52197	hemagglutinin - in
22	55	68.8	347	2 S52199	hemagglutinin - in
23	55	68.8	362	2 S38637	hemagglutinin - in
24	55	68.8	550	1 HMIW52	hemagglutinin prec
25	55	68.8	550	1 HMIW53	hemagglutinin prec
26	55	68.8	550	1 HMIW77	hemagglutinin prec
27	55	68.8	550	1 HMIW80	hemagglutinin prec
28	55	68.8	550	1 HMIW33	hemagglutinin prec
29	55	68.8	550	1 HMIW89	hemagglutinin prec

30	55	68.8	550	1 HMIW98	hemagglutinin prec
31	55	68.8	550	1 HMIW15	hemagglutinin prec
32	55	68.8	550	1 HMIW86	hemagglutinin prec
33	55	68.8	550	2 JQ1153	hemagglutinin prec
34	55	68.8	550	2 JQ1154	hemagglutinin prec
35	55	68.8	550	2 JQ1155	hemagglutinin prec
36	55	68.8	550	2 JQ1156	hemagglutinin prec
37	55	68.8	565	1 HMIWE2	hemagglutinin prec
38	55	68.8	565	1 HMIWE4	hemagglutinin prec
39	55	68.8	566	1 HMIWH	hemagglutinin prec
40	55	68.8	566	1 HMIVHA	hemagglutinin prec
41	55	68.8	566	1 HMIVHM	hemagglutinin prec
42	55	68.8	566	1 HMIW6	hemagglutinin prec
43	55	68.8	567	1 HMIWV	hemagglutinin prec
44	54	67.5	565	1 HMIWE1	hemagglutinin prec
45	54	67.5	565	1 HMIWE5	hemagglutinin prec

ALIGNMENTS

RESULT 1  
JQ2374  
hemagglutinin - influenza A virus (strain SNI289)  
C:Species: influenza A virus  
C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
C:Accession: JQ2374  
R:Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.  
J. Gen. Virol. 74, 2513-2518, 1993  
A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtain  
A:Reference number: JQ2369; MUID:94065682  
A:Accession: JQ2374  
A:Molecule type: mRNA  
A:Residues: 1-330 <ROC>  
A:Cross-references: GB:L20115  
A:Experimental source: subtype H3N2  
C:Superfamily: influenza virus hemagglutinin

Query Match 68.8%; Score 55; DB 2; Length 330;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDPA 9  
|||||  
Db 98 YPYDVPDPA 106

RESULT 2  
JQ2375  
hemagglutinin - influenza A virus (strain SNI389 and IN0190)  
C:Species: influenza A virus  
C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
C:Accession: JQ2375; JQ2376  
R:Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.  
J. Gen. Virol. 74, 2513-2518, 1993  
A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtain  
A:Reference number: JQ2369; MUID:94065682  
A:Accession: JQ2375  
A:Molecule type: mRNA  
A:Residues: 1-330 <ROC>  
A:Cross-references: GB:L20119  
A:Experimental source: subtype H3N2  
C:Superfamily: influenza virus hemagglutinin

Query Match 68.8%; Score 55; DB 2; Length 330;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDPA 9  
|||||  
Db 98 YPYDVPDPA 106



QY 1 YPYDVPDYA 9  
|||||  
Db 98 YPYDVPDYA 106

## RESULT 7

hemagglutinin - influenza A virus (isolate A/England/1/93) (fragment)

C:Species: Influenza A virus  
A:Variety: Isolate A/England/1/93  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52175  
R:Ellis, J.S.

submitted to the EMBL Data Library, October 1994

A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating

A:Reference number: S52173

A:Accession: S52175

A:Molecule type: mRNA

A:Residues: 1-347 <ELL>

A:Cross-references: EMBL:246393; NID:g609024; PIDN:CAA86528.1; PID:g940547

A:Experimental source: isolate A/England/1/93

C:Superfamily: Influenza virus hemagglutinin

Query Match 68.8%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
Db 98 YPYDVPDYA 106

## RESULT 8

hemagglutinin - influenza A virus (isolate A/England/247/93) (fragment)

C:Species: Influenza A virus  
A:Variety: Isolate A/England/247/93  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52176  
R:Ellis, J.S.

submitted to the EMBL Data Library, October 1994

A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating

A:Reference number: S52173

A:Accession: S52176

A:Molecule type: mRNA

A:Residues: 1-347 <ELL>

A:Cross-references: EMBL:246394; NID:g609025; PIDN:CAA86529.1; PID:g609026

A:Experimental source: isolate A/England/247/93

C:Superfamily: Influenza virus hemagglutinin

Query Match 68.8%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
Db 98 YPYDVPDYA 106

## RESULT 9

hemagglutinin - influenza A virus (isolate A/England/284/93) (fragment)

C:Species: Influenza A virus  
A:Variety: Isolate A/England/284/93  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52178  
R:Ellis, J.S.

submitted to the EMBL Data Library, October 1994

A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating

A:Reference number: S52173

A:Accession: S52178

A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>

A:Cross-references: EMBL:246396; NID:g609029; PIDN:CAA86531.1; PID:g609030

A:Experimental source: isolate A/England/284/93

C:Superfamily: Influenza virus hemagglutinin

Query Match 68.8%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
Db 98 YPYDVPDYA 106

## RESULT 10

hemagglutinin - influenza A virus (isolate A/England/286/93) (fragment)

C:Species: Influenza A virus

A:Variety: Isolate A/England/286/93

C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001

C:Accession: S52179

R:Ellis, J.S.

submitted to the EMBL Data Library, October 1994

A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating

A:Reference number: S52173

A:Accession: S52179

A:Molecule type: mRNA

A:Residues: 1-347 <ELL>

A:Cross-references: EMBL:246397; NID:g609031; PIDN:CAA86532.1; PID:g609032

A:Experimental source: isolate A/England/286/93

C:Superfamily: Influenza virus hemagglutinin

Query Match 68.8%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
Db 98 YPYDVPDYA 106

## RESULT 11

hemagglutinin - influenza A virus (isolate A/England/289/93) (fragment)

C:Species: Influenza A virus

A:Variety: Isolate A/England/289/93

C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001

C:Accession: S52180

R:Ellis, J.S.

submitted to the EMBL Data Library, October 1994

A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating

A:Reference number: S52173

A:Accession: S52180

A:Molecule type: mRNA

A:Residues: 1-347 <ELL>

A:Cross-references: EMBL:246398; NID:g609033; PIDN:CAA86533.1; PID:g609034

A:Experimental source: isolate A/England/289/93

C:Superfamily: Influenza virus hemagglutinin

Query Match 68.8%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
Db 98 YPYDVPDYA 106

## RESULT 12

S52182  
hemagglutinin - influenza A virus (isolate A/England/328/93) (fragment)  
C:Species: influenza A virus  
A:Variety: isolate A/England/328/93  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52182  
R:Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating influenza A virus  
A:Reference number: S52173  
A:Accession: S52182  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:Z46400; NID:g609037; PIDN:CAA86535.1; PID:g609038  
A:Experimental source: isolate A/England/346/93  
C:Superfamily: influenza virus hemagglutinin

Query Match 68.8%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | | |  
Db 98 YPYDVPDYA 106

## RESULT 13

S52183  
hemagglutinin - influenza A virus (isolate A/England/347/93) (fragment)  
C:Species: influenza A virus  
A:Variety: isolate A/England/347/93  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52183  
R:Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating influenza A virus  
A:Reference number: S52173  
A:Accession: S52183  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:Z46401; NID:g609039; PIDN:CAA86536.1; PID:g609040  
A:Experimental source: isolate A/England/347/93  
C:Superfamily: influenza virus hemagglutinin

Query Match 68.8%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | | |  
Db 98 YPYDVPDYA 106

## RESULT 14

S52185  
hemagglutinin - influenza A virus (isolate A/England/67/94) (fragment)  
C:Species: influenza A virus  
A:Variety: isolate A/England/67/94  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52185  
R:Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating influenza A virus  
A:Reference number: S52173  
A:Accession: S52185  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:Z46403; NID:g609043; PIDN:CAA86538.1; PID:g609044  
A:Experimental source: isolate A/England/67/94  
C:Superfamily: influenza virus hemagglutinin

Query Match 68.8%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 68.8%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | | |  
Db 98 YPYDVPDYA 106

## RESULT 15

S52186  
hemagglutinin - influenza A virus (isolate A/England/68/94) (fragment)  
C:Species: influenza A virus  
A:Variety: isolate A/England/68/94  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52186  
R:Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circulating influenza A virus  
A:Reference number: S52173  
A:Accession: S52186  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:Z46404; NID:g609045; PIDN:CAA86539.1; PID:g609046  
A:Experimental source: isolate A/England/68/94  
C:Superfamily: influenza virus hemagglutinin

Query Match 68.8%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
| | | | | | | | | |  
Db 98 YPYDVPDYA 106

Search completed: April 11, 2002, 10:16:16  
Job time: 126 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2002, 10:22:00 ; Search time 18.1 Seconds  
(without alignments)  
28.360 Million cell updates/sec

Title: US-09-284-787-2  
Perfect score: 80  
Sequence: 1 YPYDVPDYAGSGSK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36564827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	68.8	249	HEMA_IAX31	P03438 influenza a
2	55	68.8	328	HEMA_IAEN6	P04664 influenza a
3	55	68.8	328	HEMA_IAQU7	P04663 influenza a
4	55	68.8	550	HEMA_IABAN	P03441 influenza a
5	55	68.8	550	HEMA_IADH1	P12582 influenza a
6	55	68.8	550	HEMA_IADH2	P12583 influenza a
7	55	68.8	550	HEMA_IADH3	P12584 influenza a
8	55	68.8	550	HEMA_IADH4	P12585 influenza a
9	55	68.8	550	HEMA_IADH6	P12587 influenza a
10	55	68.8	550	HEMA_IADH7	P12588 influenza a
11	55	68.8	550	HEMA_IADHK	P43257 influenza a
12	55	68.8	550	HEMA_IADHL	P43258 influenza a
13	55	68.8	550	HEMA_IADHM	P43259 influenza a
14	55	68.8	550	HEMA_IAGHK	P43260 influenza a
15	55	68.8	550	HEMA_IAME6	P11333 influenza a
16	55	68.8	550	HEMA_IAMH2	P11334 influenza a
17	55	68.8	550	HEMA_IAMH3	P11334 influenza a
18	55	68.8	565	HEMA_IAMH4	P16994 influenza a
19	55	68.8	565	HEMA_IAMH1	P15658 influenza a
20	55	68.8	566	HEMA_IAMH2	P03437 influenza a
21	55	68.8	566	HEMA_IAMH2	P26135 influenza a
22	55	68.8	566	HEMA_IAMH7	P03440 influenza a
23	55	68.8	566	HEMA_IAMAO	P26138 influenza a
24	55	68.8	566	HEMA_IAMH1	P03449 influenza a
25	55	68.8	566	HEMA_IAMH2	P03439 influenza a
26	55	68.8	566	HEMA_IAMH6	P03436 influenza a
27	55	68.8	566	HEMA_IAMH6	P19106 influenza a
28	55	68.8	566	HEMA_IAMH6	P26139 influenza a
29	55	68.8	567	HEMA_IAMH7	P03435 influenza a
30	54	67.5	565	HEMA_IAMH7	P16995 influenza a
31	54	67.5	565	HEMA_IAMH6	P19699 influenza a
32	54	67.5	565	HEMA_IAMH7	P16996 influenza a
33	54	67.5	565	HEMA_IAMH6	P16997 influenza a

34	54	67.5	565	1	HEMA_IAMH7	P16998 influenza a
35	54	67.5	565	1	HEMA_IAMH7	P16999 influenza a
36	54	67.5	565	1	HEMA_IAMH7	P08011 influenza a
37	54	67.5	565	1	HEMA_IAMH7	P17001 influenza a
38	54	67.5	565	1	HEMA_IAMH7	P17002 influenza a
39	54	67.5	565	1	HEMA_IAMH7	P03442 influenza a
40	54	67.5	566	1	HEMA_IAMH7	P26134 influenza a
41	52.5	65.6	566	1	HEMA_IAMH7	P26141 influenza a
42	52.5	65.6	566	1	HEMA_IAMH7	P26137 influenza a
43	51.5	64.4	563	1	HEMA_IAMH7	P26136 influenza a
44	51.5	64.4	568	1	HEMA_IAMH7	P17000 influenza a
45	50	62.5	565	1	HEMA_IAMH7	P12586 influenza a

ALIGNMENTS

RESULT 1						
HEMA_IAX31						
ID	HEMA_IAX31	STANDARD;	PRT;	249	AA.	
AC	P03438;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	21-JUL-1986 (Rel. 01, Last sequence update)					
DT	20-AUG-2001 (Rel. 40, Last annotation update)					
DE	HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAL CHAIN]					
DE	(FRAGMENT).					
GN	HA.					
OS	Influenza A virus (strain X-31).					
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;					
OC	Influenza virus A and B group; Influenza A viruses;					
OC	Influenza A virus.					
OX	NCBI_TaxID=11489;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=81030852; PubMed=7421990;					
RA	Gething M.-J., Bye J., Skehel J.J., Waterfield M.;					
RT	"Cloning and DNA sequence of double-stranded copies of haemagglutinin genes from H2 and H3 strains elucidates antigenic shift and drift in human influenza virus.;"					
RL	Nature 287:301-306(1980).					
CC	-1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.					
CC	-1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAL AND HAZ) LINKED BY A DISULFIDE BOND.					
CC	-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.					
DR	PIR; A04051; HMVH.					
DR	HSP; P03437; 5HMG.					
DR	InterPro: IPR001364; Hemagglutn.					
DR	ProDom: PD000225; Hemagglutinin; 1.					
KW	Envelope protein; Hemagglutinin; Glycoprotein; Signal.					
FT	SIGNAL 1 16					
FT	CHAIN 17 >249					
FT	CARBOHYD 24 24					
FT	CARBOHYD 38 38					
FT	CARBOHYD 54 54					
FT	CARBOHYD 97 97					
FT	CARBOHYD 181 181					
FT	NON_TER 249 249					
SQ	SEQUENCE 249 AA; 27373 MW; 9537AA970BB79183 CRC64;					

Query Match 68.8%; Score 55; DB 1; Length 249;  
Best Local Similarity 100.0%; Pred. No. 0.052;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | | |  
Db 114 YPYDVPDYA 122

RESULT 2

```
HEMA_IAEN6
ID HEMA_IAEN6 STANDARD; PRT; 328 AA.
AC P04664;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HA1 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/England/878/69).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81194918; PubMed=6164798;
RA Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.;
RT "Antigenic drift in the hemagglutinin of the Hong Kong influenza
subtypes: correlation of amino acid changes with alterations in viral
antigenicity.";
RL J. Virol. 37:845-853(1981).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81194918; PubMed=6164798;
RA Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.;
RT "Antigenic drift in the hemagglutinin of the Hong Kong influenza
subtypes: correlation of amino acid changes with alterations in viral
antigenicity.";
RL J. Virol. 37:845-853(1981).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC
CC EMBL; K03335; AAA43184.1;
CC InterPro; IPR001364; Hemagglutn.
CC Pfam; PF00509; Hemagglutinin; 1.
CC ProDom; PD000225; Hemagglutn; 1.
KW Envelope protein; Hemagglutinin; Glycoprotein.
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CARBOHYD 8 22 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON_TER 328 328
SQ SEQUENCE 328 AA; 36072 MW; 9C3A86B3A8D56FE CRC64;

Query Match 68.8%; Score 55; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
Db 98 YPYDVPDYA 106
|||||||

RESULT 3
HEMA_IAOU7
ID HEMA_IAOU7 STANDARD; PRT; 328 AA.
AC P04663;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HA1 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Qu/7/70).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82033259; PubMed=6169840;
RA Both G.W., Sleigh M.J.;
RT "Conservation and variation in the hemagglutinins of Hong Kong
subtypes influenza viruses during antigenic drift.";
RL J. Virol. 39:663-672(1981).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC
CC EMBL; K03335; AAA43184.1;
CC InterPro; IPR001364; Hemagglutn.
CC Pfam; PF00509; Hemagglutinin; 1.
CC ProDom; PD000225; Hemagglutn; 1.
KW Envelope protein; Hemagglutinin; Glycoprotein.
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CARBOHYD 8 22 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON_TER 328 328
SQ SEQUENCE 328 AA; 36072 MW; 9C3A86B3A8D56FE CRC64;

Query Match 68.8%; Score 55; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
Db 98 YPYDVPDYA 106
|||||||

RESULT 4
HEMA_IABAN
ID HEMA_IABAN STANDARD; PRT; 550 AA.
AC P03441; Q83961; Q83962;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Bangkok/1/79).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11325;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82033259; PubMed=6169840;
RA Both G.W., Sleigh M.J.;
RT "Conservation and variation in the hemagglutinins of Hong Kong
subtypes influenza viruses during antigenic drift.";
RL J. Virol. 39:663-672(1981).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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or send an email to license@isb-sib.ch).
CC
CC EMBL; K03338; AAA43195.1;
CC InterPro; IPR001364; Hemagglutn.
CC Pfam; PF00509; Hemagglutinin; 1.
CC ProDom; PD000225; Hemagglutn; 1.
KW Envelope protein; Hemagglutinin; Glycoprotein.
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON_TER 328 328
SQ SEQUENCE 328 AA; 36059 MW; E30A962FD6DD805B CRC64;

Query Match 68.8%; Score 55; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
Db 98 YPYDVPDYA 106
|||||||
```

```
CC      CELL RECEPTORS AND FOR INITIATING INFECTION.
CC      -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC      (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC      -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
CC
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL: J02092; AAA43182.1; -.
CC      PIR: A04052; HMIIV6.
CC      InterPro: IPR001364; Hemagglutn.
CC      Pfam: PF00509; Hemagglutinin; 1.
CC      ProDom: PD000225; Hemagglutn; 1.
CC      Envelope protein; Hemagglutinin; Glycoprotein.
CC      NON_TER 1 1
CC      CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC      CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC      FT CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 126 126 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      SEQUENCE 550 AA; 61699 MW; FBD2EC200689CBE5 CRC64;
CC
CC      Query Match 68.8%; Score 55; DB 1; Length 550;
CC      Best Local Similarity 100.0%; Pred. No. 0.12;
CC      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 1 YPYDVDPDYA 9
CC      DB 98 YPYDVDPDYA 106
CC
CC      RESULT 5
CC      HEMA_IADH1
CC      ID HEMA_IADH1 STANDARD; PRT: 550 AA.
CC      AC P12582; Q84021; Q84022;
CC      DT 01-OCT-1989 (Rel. 12, Created)
CC      DT 01-OCT-1989 (Rel. 12, Last sequence update)
CC      DT 20-AUG-2001 (Rel. 40, Last annotation update)
CC      DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
CC      DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
CC      GN HA.
CC      OS Influenza A virus (strain A/Duck/Hokkaido/5/77).
CC      OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
CC      OC Influenza virus A and B group; Influenza A viruses;
CC      OC Influenza A virus.
CC      OX NCBI_TaxID=11357;
CC      RN [1]
CC      RP SEQUENCE FROM N.A.
CC      RX MEDLINE=87265458; PubMed=2440178;
CC      RA Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
CC      RT "Antigenic and genetic conservation of H3 influenza virus in wild
CC      RT ducks.";
CC      RL Virology 159:109-119(1987).
CC      CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC      CELL RECEPTORS AND FOR INITIATING INFECTION.
CC      CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC      (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC      CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL: M16737; AAA43143.1; -.
CC      PIR: A27813; HMIIV77.
CC      InterPro: IPR001364; Hemagglutn.
CC      Pfam: PF00509; Hemagglutinin; 1.
CC      ProDom: PD000225; Hemagglutn; 1.
CC      Envelope protein; Hemagglutinin; Glycoprotein.
CC      NON_TER 1 1
CC      CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC      CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC      FT CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      SEQUENCE 550 AA; 61705 MW; 7E7ACFE716FC969A CRC64;
CC
CC      Query Match 68.8%; Score 55; DB 1; Length 550;
CC      Best Local Similarity 100.0%; Pred. No. 0.12;
CC      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 1 YPYDVDPDYA 9
CC      DB 98 YPYDVDPDYA 106
CC
CC      RESULT 6
CC      HEMA_IADH2
CC      ID HEMA_IADH2 STANDARD; PRT: 550 AA.
CC      AC P12583; Q84011;
CC      DT 01-OCT-1989 (Rel. 12, Created)
CC      DT 01-APR-1990 (Rel. 14, Last sequence update)
CC      DT 20-AUG-2001 (Rel. 40, Last annotation update)
CC      DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
CC      DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
CC      GN HA.
CC      OS Influenza A virus (strain A/Duck/Hokkaido/8/80).
CC      OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
CC      OC Influenza virus A and B group; Influenza A viruses;
CC      OC Influenza A virus.
CC      OX NCBI_TaxID=11358;
CC      RN [1]
CC      RP SEQUENCE FROM N.A.
CC      RX MEDLINE=87265458; PubMed=2440178;
CC      RA Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
CC      RT "Antigenic and genetic conservation of H3 influenza virus in wild
CC      RT ducks.";
CC      RL Virology 159:109-119(1987).
CC      CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC      CELL RECEPTORS AND FOR INITIATING INFECTION.
CC      CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC      (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC      CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL: M16738; AAA43144.1; -.
CC      PIR: B27813; HMIIV80.
CC      InterPro: IPR001364; Hemagglutn.
CC      Pfam: PF00509; Hemagglutinin; 1.
CC      ProDom: PD000225; Hemagglutn; 1.
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KW Envelope protein; Hemagglutinin; Glycoprotein.  
FT NON\_TER 1 1 HEMAGGLUTININ HA1 CHAIN.  
FT CHAIN 1 328 HEMAGGLUTININ HA2 CHAIN.  
FT CHAIN 330 550  
FT CARBOHYD 8 8  
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 137 137 K -> N (IN PIR DATA BANK).  
SQ SEQUENCE 550 AA; 61659 MW; A107023ACC9CC353 CRC64;

Query Match 68.8%; Score 55; DB 1; Length 550;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 98 YPYDVPDYA 106  
|||||

RESULT 7  
HEMA\_IADH3  
ID HEMA\_IADH3 STANDARD; PRT; 550 AA.  
AC P12584; Q84012; Q89793;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;  
HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).  
GN HA.  
OS Influenza A virus (strain A/Duck/Hokkaido/33/80).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses;  
OC Influenza A virus.  
OX NCBI\_TaxID=11359;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87265458; PubMed=2440178;  
RA Kida H., Kawaoka Y., Naeye C.W., Webster R.G.;  
RT "Antigenic and genetic conservation of H3 influenza virus in wild  
ducks.";  
RL Virology 159:109-119(1987).  
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
CELL RECEPTORS AND FOR INITIATING INFECTION.  
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M16739; AAA43145.1; -.  
DR PIR; C27813; HMV33.  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.  
DR ProDom; PD000225; Hemagglutn; 1.  
KW Envelope protein; Hemagglutinin; Glycoprotein.  
FT NON\_TER 1 1  
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.  
FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.  
FT CARBOHYD 8 8  
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 550 AA; 61577 MW; 6C30BF67CFDCB7DE CRC64;

Query Match 68.8%; Score 55; DB 1; Length 550;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
Db 98 YPYDVPDYA 106  
|||||

RESULT 8  
HEMA\_IADH4  
ID HEMA\_IADH4 STANDARD; PRT; 550 AA.  
AC P12585; Q84013; Q84014;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;  
HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).  
GN HA.  
OS Influenza A virus (strain A/Duck/Hokkaido/7/82).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses;  
OC Influenza A virus.  
OX NCBI\_TaxID=11360;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87265458; PubMed=2440178;  
RA Kida H., Kawaoka Y., Naeye C.W., Webster R.G.;  
RT "Antigenic and genetic conservation of H3 influenza virus in wild  
ducks.";  
RL Virology 159:109-119(1987).  
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
CELL RECEPTORS AND FOR INITIATING INFECTION.  
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M16740; AAA43146.1; -.  
DR PIR; D27813; HMV89.  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.  
DR ProDom; PD000225; Hemagglutn; 1.  
KW Envelope protein; Hemagglutinin; Glycoprotein.  
FT NON\_TER 1 1  
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.  
FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.  
FT CARBOHYD 8 8  
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 550 AA; 61664 MW; A16B2CF8CBBBD9D0 CRC64;

Query Match 68.8%; Score 55; DB 1; Length 550;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
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Db 98 YPYDVPDYA 106
RESULT 9
HEMA_IADH6 STANDARD; PRT; 550 AA.
AC P12587; Q84017;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-AUG-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
GN HA.
OS Influenza A virus (strain A/Duck/Hokkaido/9/85).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11362;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87265458; PubMed=2440178;
RA Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
RT "Antigenic and genetic conservation of H3 influenza virus in wild
ducks.";
RL Virology 159:109-119(1987).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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or send an email to license@isb-sib.ch).
CC
CC EMBL; M16742; AAA43148.1; -
CC PIR; F27813; HMIV98.
CC InterPro: IPR001364; Hemagglutn.
CC Pfam: PF00509; Hemagglutinin; 1.
CC ProDom: PD000225; Hemagglutn; 1.
KW Envelope protein; Hemagglutinin; Glycoprotein.
FT NON_TER 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CHAIN 1 328 HEMAGGLUTININ HA2 CHAIN.
FT CARBOHYD 330 550 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 8 8 Y'-> N (IN PIR DATA BANK).
SQ SEQUENCE 550 AA; 61711 MW; 67BCD85F44736CFE CRC64;

Query Match 68.8%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
|||||||
Db 98 YPYDVPDYA 106

RESULT 10
HEMA_IADH7 STANDARD; PRT; 550 AA.
AC P12588; Q84018; Q89470;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
GN HA.
OS Influenza A virus (strain A/Duck/Hong Kong/7/75).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OX NCBI_TaxID=11364;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 68.8%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
|||||||
Db 98 YPYDVPDYA 106

RESULT 11
HEMA_IADHK STANDARD; PRT; 550 AA.
AC P43257;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
GN HA.
OS Influenza A virus (strain A/Duck/Hong Kong/7/75).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OX NCBI_TaxID=11364;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=91341491; PubMed=1875195;
RA Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
RT "Molecular evidence for a role of domestic ducks in the introduction
RT of avian H3 influenza viruses to pigs in southern China, where the
RT A/Hong Kong/68 (H3N2) strain emerged.";
RL J. Gen. Virol. 72:2007-2010(1991).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC
CC EMBL; D00929; BAA00769.1; -
CC HSP; P03437; 5HM;
CC InterPro: IPR001364; Hemagglutn.
CC Pfam: PF00509; Hemagglutinin; 1.
CC ProDom: PD000225; Hemagglutn; 1.
CC Envelope protein; Hemagglutinin; Glycoprotein.
CC NON_TER 1 1
CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 550 AA; 61549 MW; 864639B829FE1BA9 CRC64;
SQ
Query Match 68.8%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YPYDVPDYA 9
Db 98 YPYDVPDYA 106
RESULT 12
HEMA_IADHL STANDARD; PRT; 550 AA.
AC P43258;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hong Kong/64/76).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OC NCBI_TaxID=45412;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91341491; PubMed=1875195;
RA Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
RT "Molecular evidence for a role of domestic ducks in the introduction
RT of avian H3 influenza viruses to pigs in southern China, where the
RT A/Hong Kong/68 (H3N2) strain emerged.";
RL J. Gen. Virol. 72:2007-2010(1991).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D00929; BAA00769.1; -
CC HSP; P03437; 5HM;
CC InterPro: IPR001364; Hemagglutn.
CC Pfam: PF00509; Hemagglutinin; 1.
CC ProDom: PD000225; Hemagglutn; 1.
CC Envelope protein; Hemagglutinin; Glycoprotein.
CC NON_TER 1 1
CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 550 AA; 61549 MW; 864639B829FE1BA9 CRC64;
SQ

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CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
CC
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CC
CC EMBL; D00931; BAA00771.1; -
CC HSP; P03437; 2HM;
CC InterPro: IPR001364; Hemagglutn.
CC Pfam: PF00509; Hemagglutinin; 1.
CC ProDom: PD000225; Hemagglutn; 1.
CC Envelope protein; Hemagglutinin; Glycoprotein.
CC NON_TER 1 1
CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 550 AA; 61718 MW; A351C56789E4BE9A CRC64;
SQ
Query Match 68.8%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YPYDVPDYA 9
Db 98 YPYDVPDYA 106
RESULT 13
HEMA_IADHM STANDARD; PRT; 550 AA.
AC P43259;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hong Kong/231/77).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OC NCBI_TaxID=45411;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91341491; PubMed=1875195;
RA Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
RT "Molecular evidence for a role of domestic ducks in the introduction
RT of avian H3 influenza viruses to pigs in southern China, where the
RT A/Hong Kong/68 (H3N2) strain emerged.";
RL J. Gen. Virol. 72:2007-2010(1991).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D00931; BAA00771.1; -
CC HSP; P03437; 2HM;
CC InterPro: IPR001364; Hemagglutn.
CC Pfam: PF00509; Hemagglutinin; 1.
CC ProDom: PD000225; Hemagglutn; 1.
CC Envelope protein; Hemagglutinin; Glycoprotein.
CC NON_TER 1 1
CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 550 AA; 61718 MW; A351C56789E4BE9A CRC64;
SQ
Query Match 68.8%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YPYDVPDYA 9
Db 98 YPYDVPDYA 106

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FT	CARBOHYD		8	8	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD		22	22	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD		38	38	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD		165	165	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD		285	285	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD		483	483	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SQ	SEQUENCE	550 AA:	61676 MW:	9A1E094DA2B8ACD2 CRC64;		

  

Query Match		68.8%;	Score 55;	DB 1;	Length 550;
Best Local Similarity		100.0%;	Pred. No.	0;12;	
Matches	9;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;

  

QY	1	YPXDVPDYA	9	
Db	98	YPDVDPYA	106	

  

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RESULT 15
HEMA_IAME6
ID HEMA_IAME6 STANDARD; PRT; 550 AA.
IC PI2589;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
HA.
OS Influenza A virus (strain A/Memphis/6/86).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
ON NCBI_TaxID=11440;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88306236; PubMed=3407150;
RA Katz J.M., Webster R.G.;
RT "Antigenic and structural characterization of multiple subpopulations
of H3N2 influenza virus from an individual.";
RL Virology 165:446-456(1988).
CC -I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
-----
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entities requires a license agreement (See http://www.sib.ch/announcement/
or send an email to license@sib-sib.ch).
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CC EMBL; M21648; AAA43275.1; -.
CC PIR; A29245; HMIV86.
CC HSSP; P03437; 2HMG.
CC InterPro; IPR001364; Hemagglutn.
CC Pfam; PF00509; Hemagglutinin; 1.
CC ProDom; PD000225; Hemagglutin; 1.
CC Envelope protein; Hemagglutinin; Glycoprotein.
CC NON_TER 1
CC FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).

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SQ SEQUENCE 550 AA; 61804 MW; 52C9F14B309310ED CRC64;

Query Match 68.8%; Score 55; DB 1; Length 550;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPYDVPDYA 9  
 Db 98 YPYDVPDYA 106

Search completed: April 11, 2002, 10:22:00  
 Job time: 430 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 11, 2002, 10:22:57 ; Search time 50.04 Seconds  
(without alignments)  
40.924 Million cell updates/sec

Title: US-09-284-787-2  
Perfect score: 80  
Sequence: 1 YPYDVPDYGSGSK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL17.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	68.8	236	12 Q9W8Z1	Q9W8Z1 influenza a
2	55	68.8	236	12 Q9W8T9	Q9W8T9 influenza a
3	55	68.8	236	12 Q9W8J7	Q9W8J7 influenza a
4	55	68.8	286	12 Q9W126	Q9W126 influenza a
5	55	68.8	286	12 Q9W125	Q9W125 influenza a
6	55	68.8	286	12 Q9W124	Q9W124 influenza a
7	55	68.8	325	12 Q40774	Q40774 influenza a
8	55	68.8	325	12 Q9DL45	Q9DL45 influenza a
9	55	68.8	326	12 Q40779	Q40779 influenza a
10	55	68.8	326	12 Q40780	Q40780 influenza a
11	55	68.8	327	12 Q92324	Q92324 influenza a
12	55	68.8	327	12 Q92325	Q92325 influenza a
13	55	68.8	327	12 Q92327	Q92327 influenza a
14	55	68.8	327	12 Q9Y190	Q9Y190 influenza a
15	55	68.8	327	12 Q9Y189	Q9Y189 influenza a
16	55	68.8	327	12 Q9Y188	Q9Y188 influenza a
17	55	68.8	327	12 Q9Y187	Q9Y187 influenza a
18	55	68.8	327	12 Q9Y186	Q9Y186 influenza a
19	55	68.8	327	12 Q9Y189	Q9Y189 influenza a

20	55	68.8	327	12 Q9YRU8	Q9YRU8 influenza a
21	55	68.8	327	12 Q9YRU7	Q9YRU7 influenza a
22	55	68.8	327	12 Q9YRU6	Q9YRU6 influenza a
23	55	68.8	327	12 Q9YRU5	Q9YRU5 influenza a
24	55	68.8	327	12 Q9YRU4	Q9YRU4 influenza a
25	55	68.8	327	12 Q9YRU3	Q9YRU3 influenza a
26	55	68.8	327	12 Q9YJ57	Q9YJ57 influenza a
27	55	68.8	327	12 Q9YIN9	Q9YIN9 influenza a
28	55	68.8	327	12 Q90884	Q90884 influenza a
29	55	68.8	328	12 Q40855	Q40855 influenza a
30	55	68.8	328	12 Q40867	Q40867 influenza a
31	55	68.8	328	12 Q82567	Q82567 influenza a
32	55	68.8	328	12 Q82568	Q82568 influenza a
33	55	68.8	328	12 Q82569	Q82569 influenza a
34	55	68.8	328	12 Q82578	Q82578 influenza a
35	55	68.8	328	12 Q82579	Q82579 influenza a
36	55	68.8	328	12 Q82580	Q82580 influenza a
37	55	68.8	328	12 Q82581	Q82581 influenza a
38	55	68.8	328	12 Q82575	Q82575 influenza a
39	55	68.8	328	12 Q82576	Q82576 influenza a
40	55	68.8	328	12 Q82577	Q82577 influenza a
41	55	68.8	328	12 Q82582	Q82582 influenza a
42	55	68.8	328	12 Q82583	Q82583 influenza a
43	55	68.8	328	12 Q82586	Q82586 influenza a
44	55	68.8	328	12 Q82587	Q82587 influenza a
45	55	68.8	328	12 Q82589	Q82589 influenza a

ALIGNMENTS

RESULT 1  
Q9W8Z1 ID Q9W8Z1 PRELIMINARY; PRT; 236 AA.  
AC Q9W8Z1;  
DT 01-NOV-1999 (TREMREL. 12, Created)  
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)  
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)  
DE HEMAGGLUTININ (FRAGMENT).  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OX Influenza virus A and B group; Influenza A viruses.  
NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-TOKYO1527, TOKYO1511;  
RA Mori S., Sekine H.;  
RT "HA1 domain of Influenza A (H3N2) virus."  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB013807; BAA77285.1; -.  
DR EMBL; AB013806; BAA77284.1; -.  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.  
DR PRINTS; PR00329; HEMAGGLUTN12.  
DR PRODom; PD000225; Hemagglutn; 1.  
DR NON\_TER 1  
FT NON\_TER 236  
SQ SEQUENCE 236 AA; 26477 MW; 4566C8E7210FB558 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
|||||  
DB 11 YPYDVPDYA 19

RESULT 2  
Q9W8T9 ID Q9W8T9 PRELIMINARY; PRT; 236 AA.  
AC Q9W8T9;

DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEMAGGLUTININ (FRAGMENT).  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-TOKYO1570, TOKYO1566, TOKYO1567, TOKYO1568, TOKYO1569;  
RA Mori S., Sekine H.;  
RT "HA1 domain of Influenza A (H3N2) virus.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB013813; BAA77291.1; -  
DR EMBL; AB013809; BAA77287.1; -  
DR EMBL; AB013810; BAA77288.1; -  
DR EMBL; AB013811; BAA77289.1; -  
DR EMBL; AB013812; BAA77290.1; -  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.  
DR PRINTS; PR00329; HEMAGGLUTN12.  
DR PRODOM; PD000225; Hemagglutn; 1.  
FT NON\_TER 1  
FT NON\_TER 236  
SQ SEQUENCE 236 AA; 26491 MW; 44CD257210FB558 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | |  
DB 11 YPYDVPDYA 19

RESULT 3  
Q9W8J7 ID Q9W8J7 PRELIMINARY; PRT; 236 AA.  
AC Q9W8J7  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEMAGGLUTININ (FRAGMENT).  
GN HA.  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-72, 70, AND 71;  
RA Nagashima M., Mori S., Sekine H.;  
RT "Influenza A virus gene for hemagglutinin.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-TOKYO1539;  
RA Mori S., Sekine H.;  
RT "HA1 domain of Influenza A (H3N2) virus.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB014062; BAA77294.1; -  
DR EMBL; AB013808; BAA77286.1; -  
DR EMBL; AB014060; BAA77292.1; -  
DR EMBL; AB014061; BAA77293.1; -  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.  
DR PRINTS; PR00329; HEMAGGLUTN12.  
DR PRODOM; PD000225; Hemagglutn; 1.  
FT NON\_TER 1  
FT NON\_TER 236  
SQ SEQUENCE 236 AA; 26493 MW; 457455682C8D28D7 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | |  
DB 11 YPYDVPDYA 19

RESULT 4  
Q9WI26 ID Q9WI26 PRELIMINARY; PRT; 286 AA.  
AC Q9WI26  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE H3 HEMAGGLUTININ (FRAGMENT).  
GN HA.  
OS Influenza A virus (A/Taiwan/2034/96(H3N2)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.  
OX NCBI\_TaxID=95241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A/TAIWAN/2034/96;  
RA Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;  
RT "Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in Taiwan.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF139937; AAD34854.1; -  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.  
DR PRINTS; PR00329; HEMAGGLUTN12.  
DR PRODOM; PD000225; Hemagglutn; 1.  
FT NON\_TER 1  
FT NON\_TER 286  
SQ SEQUENCE 286 AA; 32075 MW; 7BA39C7632D33186 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 286;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | |  
DB 57 YPYDVPDYA 65

RESULT 5  
Q9WI25 ID Q9WI25 PRELIMINARY; PRT; 286 AA.  
AC Q9WI25  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE H3 HEMAGGLUTININ (FRAGMENT).  
GN HA.  
OS Influenza A virus (A/Taiwan/2192/96(H3N2)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.  
OX NCBI\_TaxID=95240;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A/TAIWAN/2192/96;  
RA Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;  
RT "Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in Taiwan.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF139936; AAD34853.1; -  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.

DR PRINTS: PR00329; HEMAGGLUTN12.  
DR PRODOM: PD000225; Hemagglutn; 1.  
FT NON\_TER 1  
FT 286  
SQ SEQUENCE 286 AA; 32059 MW; CB51B092AAD0D7D8 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 286;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | |  
DB 57 YPYDVPDYA 65

RESULT 6

ID Q9WI24 PRELIMINARY; PRT; 286 AA.  
AC Q9WI24;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE H3 HEMAGGLUTININ (FRAGMENT).  
GN HA.  
OS Influenza A virus (A/Taiwan/2191/96(H3N2)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.  
OX NCBI\_TaxID=95236;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/TAIWAN/2191/96;  
RA Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;  
RT "Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in Taiwan";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF139932; AAD34849.1; -.  
DR InterPro: IPR001364; Hemagglutn.  
DR Pfam: PF00509; Hemagglutinin; 1.  
DR PRINTS: PR00329; HEMAGGLUTN12.  
DR PRODOM: PD000225; Hemagglutn; 1.  
FT NON\_TER 1  
FT 286  
SQ SEQUENCE 286 AA; 31976 MW; 59AB2AE727D26078 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 286;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | |  
DB 57 YPYDVPDYA 65

RESULT 7

ID O40774 PRELIMINARY; PRT; 325 AA.  
AC O40774;  
DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE HEMAGGLUTININ GENE (FRAGMENT).  
GN HA.  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/ILLINOIS/5/95(H3N2);  
RA Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF008782; AAB63719.1; -.  
DR InterPro: IPR001364; Hemagglutn.  
DR Pfam: PF00509; Hemagglutinin; 1.  
DR PRODOM: PD000225; Hemagglutn; 1.  
FT NON\_TER 1  
FT 325  
SQ SEQUENCE 325 AA; 36103 MW; 4E5B4648C2024765 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 325;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | |  
DB 98 YPYDVPDYA 106

RESULT 8

ID Q9DL45 PRELIMINARY; PRT; 325 AA.  
AC Q9DL45;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE HEMAGGLUTININ (FRAGMENT).  
OS Influenza A virus (A/Finland/583/98(H3N2)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.  
OX NCBI\_TaxID=147149;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/FINLAND/583/98;  
RA Pyhala R., Haanpaa M., Kleemola M., Tervahauta R., Visakorpi R., Kinnunen L.;  
RT "Acceptable protective efficacy of influenza vaccination in young military conscripts in circumstances of incomplete antigenic and genetic match.";  
RL Vaccine 0:0-0(2001).  
DR EMBL: AF311689; AAG47810.1; -.  
DR InterPro: IPR001364; Hemagglutn.  
DR Pfam: PF00509; Hemagglutinin; 1.  
DR PRINTS: PR00329; HEMAGGLUTN12.  
DR PRODOM: PD000225; Hemagglutn; 1.  
FT NON\_TER 1  
FT 325  
SQ SEQUENCE 325 AA; 36029 MW; 5BECB8CC3E83B1C2 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 325;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | |  
DB 98 YPYDVPDYA 106

RESULT 9

ID O40779 PRELIMINARY; PRT; 326 AA.  
AC O40779;  
DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE HEMAGGLUTININ GENE (FRAGMENT).  
GN HA.  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-A/NEW\_YORK/28/94(H3N2);  
RA Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF008787; AAC63724.1; -  
DR InterPro: IPR001364; Hemagglutn.  
DR Pfam: PF00509; Hemagglutinin; 1.  
DR ProDom: PD000225; Hemagglutn; 1.  
FT NON\_TER 1 326  
FT SEQUENCE 326 AA; 36197 MW; 4B84BD4AADCA4A77 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 326;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | | |  
Db 98 YPYDVPDYA 106

RESULT 10  
O40780  
ID O40780 PRELIMINARY; PRT; 326 AA.  
AC O40780;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEMAGGLUTININ GENE (FRAGMENT).  
GN HA.  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A/PENNSYLVANIA/7/94(H3N2);  
RA Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF008788; AAC63725.1; -  
DR InterPro: IPR001364; Hemagglutn.  
DR Pfam: PF00509; Hemagglutinin; 1.  
DR ProDom: PD000225; Hemagglutn; 1.  
FT NON\_TER 1 326  
FT SEQUENCE 326 AA; 36349 MW; 6A11A4CBBFBD6CC9 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 326;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | | |  
Db 98 YPYDVPDYA 106

RESULT 11  
O92324  
ID O92324 PRELIMINARY; PRT; 327 AA.  
AC O92324;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEMAGGLUTININ (FRAGMENT).  
GN HA.  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A/SYDNEY/05/97-LIKE(H3N2);

RA Oslowy C.K.;  
RT "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus  
isolates circulating in Canada during the 1997/98 Influenza season.";  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF087700; AAC36729.1; -  
DR InterPro: IPR001364; Hemagglutn.  
DR Pfam: PF00509; Hemagglutinin; 1.  
DR ProDom: PD000225; Hemagglutn; 1.  
FT NON\_TER 1 327  
FT SEQUENCE 327 AA; 36389 MW; 909239953649069B CRC64;

Query Match 68.8%; Score 55; DB 12; Length 327;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | | |  
Db 98 YPYDVPDYA 106

RESULT 12  
O92325  
ID O92325 PRELIMINARY; PRT; 327 AA.  
AC O92325;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEMAGGLUTININ (FRAGMENT).  
GN HA.  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A/SYDNEY/05/97-LIKE(H3N2);  
RA Oslowy C.K.;  
RT "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus  
isolates circulating in Canada during the 1997/98 Influenza season.";  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF087703; AAC36732.1; -  
DR InterPro: IPR001364; Hemagglutn.  
DR Pfam: PF00509; Hemagglutinin; 1.  
DR ProDom: PD000225; Hemagglutn; 1.  
FT NON\_TER 1 327  
FT SEQUENCE 327 AA; 36457 MW; D741E3C39D0C4D6A CRC64;

Query Match 68.8%; Score 55; DB 12; Length 327;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
| | | | | | | | | |  
Db 98 YPYDVPDYA 106

RESULT 13  
O92327  
ID O92327 PRELIMINARY; PRT; 327 AA.  
AC O92327;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEMAGGLUTININ (FRAGMENT).  
GN HA.  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses.  
OX NCBI\_TaxID=11320;

```

RN RP SEQUENCE FROM N.A.
RC STRAIN=A/SYDNEY/05/97(H3N2);
RA Oslowy C.K.;
RT "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
RL Isolates circulating in Canada during the 1997/98 Influenza season.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF087709; AAC36738.1; -
DR InterPro: IPR001364; Hemagglutn.
DR Pfam: PF00509; Hemagglutinin; 1.
DR ProDom: PD000225; Hemagglutn; 1.
DR NON_TER 1
FT NON_TER 327
SQ SEQUENCE 327 AA; 36293 MW; 4A72007829B091F5 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
Db 98 YPYDVPDYA 106

RESULT 14
Q9YT90 PRELIMINARY; PRT; 327 AA.
AC Q9YT90;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HEMAGGLUTININ (FRAGMENT).
GN HA.
OS Influenza A virus (A/Sydney/05/97-like(H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=82372;

RN RP SEQUENCE FROM N.A.
RC STRAIN=A/SYDNEY/05/97-LIKE(H3N2);
RA Oslowy C.K.;
RT "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
RL Isolates circulating in Canada during the 1997/98 Influenza season.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF087702; AAC36731.1; -
DR InterPro: IPR001364; Hemagglutn.
DR Pfam: PF00509; Hemagglutinin; 1.
DR ProDom: PD000225; Hemagglutn; 1.
DR NON_TER 1
FT NON_TER 327
SQ SEQUENCE 327 AA; 36446 MW; 9E9FA8433CFC1B01 CRC64;

Query Match 68.8%; Score 55; DB 12; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9
Db 98 YPYDVPDYA 106

```

Query Match 68.8%; Score 55; DB 12; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 0.36;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 Db 98 YPYDVPDYA 106

Search completed: April 11, 2002, 10:22:57  
 Job time: 427 sec

Query Match 68.8%; Score 55; DB 12; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 0.36;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPYDVPDYA 9  
 Db 98 YPYDVPDYA 106

```

RESULT 15
Q9YT89 PRELIMINARY; PRT; 327 AA.
AC Q9YT89;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HEMAGGLUTININ (FRAGMENT).
GN HA.

```

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2002, 10:15:43 ; Search time 53.05 Seconds  
(without alignments)  
18.152 Million cell updates/sec

Title: US-09-284-787-3

Perfect score: 75

Sequence: 1 SGSGPYDVPDYA 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*

- 1: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT.\*
- 2: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /SIDSB/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 7: /SIDSB/gcgdata/geneseq/geneseq/AA1986.DAT.\*
- 8: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT.\*
- 9: /SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT.\*
- 10: /SIDSB/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 11: /SIDSB/gcgdata/geneseq/geneseq/AA1990.DAT.\*
- 12: /SIDSB/gcgdata/geneseq/geneseq/AA1991.DAT.\*
- 13: /SIDSB/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SIDSB/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT.\*
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- 19: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT.\*
- 22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	13	19 AAW59452	Human influenza vi
2	71	94.7	34	21 AAB07730	Peptide encoded by
3	67	89.3	17	18 AAW41032	Flu-epitope scamb
4	67	89.3	17	18 AAW29116	Flu epitope tagged
5	67	89.3	17	22 AAB45969	Transdominant effe
6	67	89.3	19	21 AAY90725	Influenza haemaggl
7	67	89.3	38	20 AAY49751	Compact structure
8	65	86.7	16	21 AAB03963	PTAT-HA linker pol
9	65	86.7	16	21 AAB29443	PTAT-HA linker-enc
10	64	86.0	165	22 AAG63606	Amino acid sequenc
11	62	82.7	481	18 AAW27158	Saccharomyces cere

12	61	81.3	10	20	AAW73372	Haemagglutinin epi
13	61	81.3	11	20	AAW73371	Haemagglutinin epi
14	61	81.3	11	22	AAW73290	Haemagglutinin, HA
15	61	81.3	12	20	AAW73370	Haemagglutinin epi
16	61	81.3	12	22	AAW49724	Influenza haemaglu
17	61	81.3	80	21	AAW97533	Truncated Human p2
18	61	81.3	80	21	AAW96048	Truncated cyclin d
19	61	81.3	80	21	AAW96075	Human cyclin depen
20	61	81.3	177	21	AAW97530	Truncated Human p2
21	61	81.3	177	21	AAW96045	Human truncated cy
22	61	81.3	177	21	AAW96072	Human cyclin depen
23	61	81.3	224	22	AAW99371	Human interleukin
24	61	81.3	224	22	AAW99372	Human interleukin
25	61	81.3	224	22	AAW99373	Human interleukin
26	61	81.3	224	22	AAW99375	Human interleukin
27	61	81.3	224	22	AAW99377	Human interleukin
28	61	81.3	224	22	AAW99379	Human interleukin
29	61	81.3	224	22	AAW99392	Human interleukin
30	61	81.3	224	22	AAW99393	Human interleukin
31	61	81.3	224	22	AAW99395	Human interleukin
32	61	81.3	224	22	AAW99396	Human interleukin
33	61	81.3	224	22	AAW99398	Human interleukin
34	61	81.3	224	22	AAW99399	Human interleukin
35	61	81.3	224	22	AAW75004	Anti-IL8 monoclonal
36	61	81.3	224	22	AAW75005	Anti-IL8 monoclonal
37	61	81.3	224	22	AAW75006	Anti-IL8 monoclonal
38	61	81.3	224	22	AAW75008	Anti-IL8 monoclonal
39	61	81.3	224	22	AAW75010	Anti-IL8 monoclonal
40	61	81.3	224	22	AAW75012	Anti-IL8 monoclonal
41	61	81.3	224	22	AAW75025	Anti-IL8 monoclonal
42	61	81.3	224	22	AAW75026	Anti-IL8 monoclonal
43	61	81.3	224	22	AAW75028	Anti-IL8 monoclonal
44	61	81.3	224	22	AAW75029	Anti-IL8 monoclonal
45	61	81.3	224	22	AAW75031	Anti-IL8 monoclonal

ALIGNMENTS

RESULT 1  
AAW59452  
ID AAW59452 standard; peptide; 13 AA.  
XX  
AC AAW59452;  
XX  
DT 28-AUG-1998 (first entry)  
XX  
DE Human influenza virus haemagglutinin epitope peptide fragment #3.  
XX  
KW Haemagglutinin; epitope; monoclonal antibody; detection; isolation;  
KW fusion protein.  
XX  
OS Human parainfluenza virus.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "N-terminal biotinyl-epsilon-Aca group"  
FT Modified-site 13 /note= "C-terminal amide group"  
FT Modified-site 13 /note= "C-terminal amide group"  
XX  
PN DE19643314-Al.  
XX  
PD 23-APR-1998.  
XX  
PF 21-OCT-1996; 96DE-1043314.  
XX  
PR 21-OCT-1996; 96DE-1043314.  
XX  
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX PTAT-HA linker pol  
XX PTAT-HA linker-enc  
XX Amino acid sequenc  
XX Saccharomyces cere  
DR WPI; 1998-241603/22.





Db 2 gggypydvdpda 13

RESULT 4  
AAW29116  
ID AAW29116 standard; Peptide; 17 AA.  
XX  
AC AAW29116;  
XX  
DT 04-FEB-1998 (first entry)  
XX  
DE  
XX  
Flu epitope tagged scrambled peptide.  
XX  
Transdominant intracellular effector peptide; RNA; screening;  
KW altered phenotype; retrovirus; library; signal transduction;  
KW antitumour; pBABE; Influenza virus; flu; epitope.  
XX  
OS Synthetic.  
XX  
PN WO9727212-A1.  
XX  
PD  
XX  
PF 31-JUL-1997.  
XX  
PF 23-JAN-1997; 97WO-US01019.  
XX  
PR 23-JAN-1996; 96US-0589911.  
PR 23-JAN-1996; 96US-0589109.  
XX  
(RIGE-) RIGEL PHARM INC.  
XX  
PI NoIn GP;  
XX  
DR WPI; 1997-393611/36.  
XX  
Screening for transdominant intracellular active agents able to  
PT alter cell phenotype - useful for examining for changed phenotype,  
PT particularly to identify potential drugs with e. g. antitumour  
PT activity  
XX  
PS Example 1; Page 53; 91pp; English.  
XX  
This peptide comprises a Flu epitope tagged scrambled peptide.  
CC Murine 10T1/2 Clone 8 cells were infected with pBABE puro  
CC retrovirus constructs containing a sequence coding for the Flu  
CC scrambled epitope or an inhibitor peptide (see AAW29117) identical  
CC to the C2 region of protein kinase C (PKA) isozymes. Control clone  
CC 8 cells showed predominantly cytoplasmic and perinuclear staining,  
CC while PMA induced cells showed translocation to the nucleus. Cells  
CC infected with constructs coding for the scrambled peptide showed  
CC similar staining. Those infected with constructs coding for  
CC the C2 region showed predominantly cytoplasmic and perinuclear  
CC staining in both control and PMA induced cells. Novel outcomes can  
CC occur upon expression of peptides in cells. A claimed method of  
CC screening for transdominant intracellular bioactive agents (A) able  
CC to alter the phenotype of a cell comprises: (a) introducing a  
CC library of different randomised nucleic acids (I) into cells; and  
CC (b) screening the cells for altered phenotype due to presence of  
CC (A). Also new are: (1) a library of retroviruses containing  
CC different randomised (I); and (2) a library of mammalian cells  
CC containing the library of (1), preferably integrated into the  
CC genome.  
XX  
SQ Sequence 17 AA;

Query Match 89.3%; Score 67; DB 18; Length 17;  
Best Local Similarity 91.7%; Pred. No. 0.00038;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGCYPYDVDPDA 13  
| | | | | | | | | |  
Db 2 gggypydvdpda 13

RESULT 6  
AAW290725  
ID AAW290725 standard; peptide; 19 AA.  
XX  
AC AAW290725;  
XX  
DT 16-AUG-2000 (first entry)  
XX

RESULT 5  
AAB45969  
ID AAB45969 standard; Peptide; 17 AA.  
XX  
AC AAB45969;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE  
XX  
Transdominant effector peptide associated screening peptide #49.  
XX  
Intracellular transdominant bioactive agent; screening; cell phenotype;  
KW effector peptide.  
XX  
OS Unidentified.  
XX  
PN US6153380-A.  
XX  
PD 28-NOV-2000.  
XX  
PF 23-JAN-1997; 97US-0789333.  
XX  
PR 23-JAN-1996; 96US-0589108.  
PR 23-JAN-1996; 96US-0589911.  
XX  
(STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (RIGE-) RIGEL PHARM INC.  
XX  
PI Rothenberg SM, Nolan GP;  
XX  
DR WPI; 2001-060084/07.  
XX  
Methods for screening intracellular transdominant effector peptides and  
PT RNA molecules comprise delivering random oligonucleotides to cells,  
PT which are then screened for an altered phenotype -  
XX  
PS Example 1; Column 79-80; 57pp; English.  
XX  
This invention describes novel in vitro screening methods (I) for a  
CC transdominant intracellular bioactive agent capable of altering the  
CC phenotype of a cell. (I) comprises: (a) introducing a molecular library  
CC of randomized candidate nucleic acids into several cells; and (b)  
CC screening the cells for a cell exhibiting an altered phenotype, where the  
CC altered phenotype is due to the presence of a transdominant bioactive  
CC agent. The methods are particularly useful for screening intracellular  
CC transdominant effector peptides and RNA molecules selected inside living  
CC cells from randomized pools. (I) is also useful for introducing random  
CC libraries into cells to screen for bioactive compounds. The methods allow  
CC rapid and highly efficient screening of large numbers of random  
CC oligonucleotides and their corresponding expression products in a single  
CC step. In addition, the methods allow screening in the absence of  
CC significant prior characterization of the cellular defect.  
XX  
SQ Sequence 17 AA;

Query Match 89.3%; Score 67; DB 22; Length 17;  
Best Local Similarity 91.7%; Pred. No. 0.00038;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGCYPYDVDPDA 13  
| | | | | | | | | |  
Db 2 gggypydvdpda 13

DE Influenza haemagglutinin epitope tag containing 19mer peptide.  
XX Fusion; scaffold protein; peptide library; green fluorescent protein;  
KW GFP; self-binding; detection; cellular expression; screening; catabolism.  
XX Influenza virus.  
XX WO200020574-A2.  
XX 13-APR-2000.  
XX 08-OCT-1999; 99WO-US23715.  
XX 08-OCT-1998; 98US-0169015.  
XX (RIGE-) RIGEL PHARM INC.  
XX Anderson D, Bogenberger JM, Peelle BR;  
XX WPI; 2000-303765/26.  
XX Fusions of scaffold proteins with random peptide libraries for improved  
XX library screening -  
XX Example 2; Page 80; 89pp; English.  
XX The present invention describes a library (X) of fusion nucleic acids,  
XX each comprising a nucleic acid encoding a random peptide, a nucleic  
XX acid encoding a scaffold protein and a nucleic acid encoding a fusion  
XX partner (the nucleic acid encoding the random peptide is inserted  
XX internally into the scaffold protein nucleic acid). Also described are:  
XX (1) a library of retroviral vectors comprising (X); (2) a library of  
XX host cells comprising (X); and (3) a method (METHOD) of screening for  
XX bioactive peptides conferring a particular phenotype, comprising  
XX providing cells containing (X). The constructs may be used in the  
XX screening of peptide libraries. The use of the scaffold proteins  
XX (especially green fluorescent protein-(GFP)) in the fusion constructs  
XX increases cellular expression levels, increases conformational stability  
XX relative to linear peptides, decreases cellular catabolism, and  
XX increases the steady state concentrations of the random peptides and  
XX random peptide library members expressed in cells for the purposes of  
XX detecting them. The present sequence represents a peptide which  
XX comprises the influenza haemagglutinin (HA) epitope tag embedded with  
XX glycines, which is used in an example from the present invention.  
XX Sequence 19 AA;

Query Match 89.3%; Score 67; DB 21; Length 19;  
Best Local Similarity 91.7%; Pred. No. 0.00042;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPPDVPDYA 13  
Db 2 GSGYPPDVPDYA 13

RESULT 7  
AAV49751  
ID AAY49751 standard; peptide; 38 AA.  
XX AC AAY49751;  
XX 19-JAN-2000 (first entry)  
XX DE Compact structure forming exemplification peptide #44.

XX Compact structure forming peptide; dimerisation; stability; scaffold;  
KW library screening; drug screening; gene therapy.  
XX Synthetic.  
XX WO9951625-A2.  
PN

XX 14-OCT-1999.  
XX 02-APR-1999; 99WO-US07374.  
XX 02-APR-1998; 98US-0080444.  
XX (RIGE-) RIGEL PHARM INC.  
XX Anderson D;  
XX WPI; 1999-620191/53.  
XX Novel dimerization peptides which self-associate are used with other  
XX proteins to effect the formation of compact structures -  
XX Disclosure; Page 13; 75pp; English.  
XX The present invention describes peptides which have a moderate or high  
XX affinity for each other, when added as extensions to both the N-terminus  
XX and C-terminus of a protein, can be used to help fold the protein into  
XX a compact structure. This compact structure is more stable to proteases.  
XX A composition (A) comprises at least a first dimerisation peptide (I)  
XX comprising the sequence (S1) that is no more than 8 amino acids long,  
XX where the composition optionally comprises a second dimerisation peptide  
XX (II): NH2-X1-X2-X3-X4-X5-COOH (S1) where X1 to X4 = Ala, Val, Ile, Leu,  
XX Trp, Phe, Met, or Tyr, and X5 = Lys, Arg, Asp or Glu;  
XX NH2-X1-X2-X3-X4-X5-COOH (II). The compositions of the invention are  
XX displayed intracellularly or extracellularly and are useful to identify  
XX binding proteins and molecules, and to modulate intracellular signalling  
XX pathways. A library of constrained proteins may be evaluated in vivo for  
XX its bioactive potential. The invention can be used to access molecules  
XX or targets within living cells, and then provide for the isolation of  
XX the constrained protein which has a phenotypic effect on the living  
XX cells. The methods are also useful to identify in vitro binding partners  
XX of the constrained protein. The compositions of the invention are useful  
XX as a scaffold for gene therapy and for potential use as a therapeutic  
XX in physiological fluids. The present sequence is used in the  
XX exemplification of the present invention.  
XX Sequence 38 AA;

Query Match 89.3%; Score 67; DB 20; Length 38;  
Best Local Similarity 91.7%; Pred. No. 0.00087;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPPDVPDYA 13  
Db 11 GSGYPPDVPDYA 22

RESULT 8  
AAB03963  
ID AAB03963 standard; Peptide; 16 AA.  
XX AC AAB03963;

XX 26-FEB-2001 (first entry)  
XX DE PTAT-HA linker polypeptide.

XX Chimeric protein; fusion protein; FLICE like inhibitor protein;  
KW FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;  
KW tumour specific antigen; immune response; therapy; prophylaxis;  
KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;  
KW acquired immune deficiency syndrome.

XX Human immunodeficiency virus.  
XX WO200059935-A1.  
XX 12-OCT-2000.  
PD





PT Transgenic animal expressing epitope-tagged TATA-box binding protein  
PT - for isolating higher-order transcription complexes and specific  
PT factors that associate with the protein, useful as potential  
PT therapeutic agents  
XX  
PS Claim 17; Page 18; 38pp; English.  
XX  
CC This sequence represents a haemagglutinin epitope. It was used in an  
CC epitope-tagged TATA-box binding protein (TBP) that is expressed by the  
CC transgenic non-human animals of the invention. The animals are used to  
CC produce TBP. TBP is used to isolate and characterise higher-order  
CC transcription complexes (from different tissue and cell types, optionally  
CC at different developmental stages). It is also used to identify new  
CC and/or specific TBP associated factors (TAFs, e.g. transcription factors,  
CC activators or inhibitors) and TAF-interaction factors, and to raise  
CC antibodies against TBP. The TAFs may be useful for regulating gene  
CC expression, e.g. disease-related genes, so are potential pharmaceuticals,  
CC also for identifying human analogues for use in drug screening. The  
CC antibodies are used for affinity purification of TBP and its complexes.  
CC TBP can isolate transcription complexes from a wide variety of different  
CC tissues and cells (contrast known methods that are limited to isolation  
CC from a particular cell type).  
XX  
SQ Sequence 10 AA;

Query Match 81.3%; Score 61; DB 20; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0019;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYPYDVDPYA 13  
|||||  
DB 1 GYPYDVDPYA 10

RESULT 13  
AAW73371  
ID AAW73371 standard; peptide; 11 AA.  
XX  
AC AAW73371;  
XX  
DT 12-FEB-1999 (first entry)  
XX  
DE Haemagglutinin epitope.  
XX  
KW TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF;  
KW TBP associated factor; TAF-interaction factor; gene expression regulator;  
KW haemagglutinin.  
XX  
OS Influenza virus.  
XX  
PN EP881288-A1.  
XX  
PD 02-DEC-1998.  
XX  
PF 26-MAY-1998; 98EP-0109516.  
XX  
PR 26-MAY-1997; 97EP-0108433.  
XX  
PA (FARH ) HOECHST AG.  
XX  
PI Berglund E, Kirschbaum B, Meisterernst M, Polites G;  
XX  
DR WPI; 1999-001394/01.  
XX  
CC Transgenic animal expressing epitope-tagged TATA-box binding protein  
CC - for isolating higher-order transcription complexes and specific  
CC factors that associate with the protein, useful as potential  
CC therapeutic agents  
XX  
PS Claim 17; Page 18; 38pp; English.  
XX  
CC This sequence represents a haemagglutinin epitope. It was used in an

CC epitope-tagged TATA-box binding protein (TBP) that is expressed by the  
CC transgenic non-human animals of the invention. The animals are used to  
CC produce TBP. TBP is used to isolate and characterise higher-order  
CC transcription complexes (from different tissue and cell types, optionally  
CC at different developmental stages). It is also used to identify new  
CC and/or specific TBP associated factors (TAFs, e.g. transcription factors,  
CC activators or inhibitors) and TAF-interaction factors, and to raise  
CC antibodies against TBP. The TAFs may be useful for regulating gene  
CC expression, e.g. disease-related genes, so are potential pharmaceuticals,  
CC also for identifying human analogues for use in drug screening. The  
CC antibodies are used for affinity purification of TBP and its complexes.  
CC TBP can isolate transcription complexes from a wide variety of different  
CC tissues and cells (contrast known methods that are limited to isolation  
CC from a particular cell type).  
XX  
SQ Sequence 11 AA;

Query Match 81.3%; Score 61; DB 20; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYPYDVDPYA 13  
|||||  
DB 2 GYPYDVDPYA 11

RESULT 14  
AAW73290  
ID AAW73290 standard; Peptide; 11 AA.  
XX  
AC AAW73290;  
XX  
DT 29-MAY-2001 (first entry)  
XX  
DE Haemagglutinin, HA, peptide tag.  
XX  
KW CREB; HA peptide tag; transgenic mouse; transcription factor;  
KW congestive heart failure; CHF; haemagglutinin.  
XX  
OS Influenza virus.  
XX  
PN US6194632-B1.  
XX  
PD 27-FEB-2001.  
XX  
PF 18-DEC-1998; 98US-0215098.  
XX  
PR 18-DEC-1997; 97US-0068011.  
XX  
PA (LEID/) LEIDEN J M.  
XX  
PI Leiden JM;  
XX  
DR WPI; 2001-256289/26.  
XX  
PT Transgenic mice expressing CREB, useful as genetic models for  
PT congestive heart failure, e.g. progressive biventricular failure,  
PT cardiac dilation, decreased myocardial contractility, peripheral edema  
PT or intracardiac thrombi  
XX  
PS Disclosure; Fig 5; 19pp; English.  
XX  
CC The present invention relates to transgenic mice comprising a transgene  
CC under operational control of a myocyte-specific promoter. The transgene  
CC encodes a protein having wild-type CREB activity or dominant negative  
CC CREB activity. CREB is a 43 kD basic leucine zipper transcription factor.  
CC The expression of the transgene leads to congestive heart failure (CHF).  
CC The transgenic mice are useful as genetic models of dilated  
CC cardiomyopathy or phenotypes associated with CHF. The transgenic mice are  
CC also useful for providing important basic information concerning the role  
CC of the CREB transcriptional pathway in regulating cardiac myocyte  
CC function. These animals will also facilitate studies designed to identify

CC new drugs that can decrease the morbidity and mortality associated with  
CC the disease. The present sequence is influenza haemagglutinin (HA)  
CC peptide tag, which was used in the present invention.

XX Sequence 11 AA;

Query Match 81.3%; Score 61; DB 22; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYPYDVPDYA 13  
| | | | |  
Db 2 gpydyvpdy 11

## RESULT 15

AAW73370  
ID AAW73370 standard; peptide; 12 AA.

XX AAW73370;

DT 12-FEB-1999 (first entry)

XX Haemagglutinin epitope.

XX TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF;  
KW TBP associated factor; TAF-interaction factor; gene expression regulator;  
KW haemagglutinin.

XX Influenza virus.

XX EP81288-A1.

XX 02-DEC-1998.

XX 26-MAY-1998; 98EP-0109516.

XX 26-MAY-1997; 97EP-0108433.

XX (FARH ) HOECHST AG.

XX Berglund E, Kirschbaum B, Meisterernst M, Polites G;

XX WPI; 1999-001394/01.

XX Transgenic animal expressing epitope-tagged TATA-box binding protein  
PT for isolating higher-order transcription complexes and specific  
PT factors that associate with the protein, useful as potential  
PT therapeutic agents

XX Claim 17; Page 16; 38pp; English.

XX This sequence represents a haemagglutinin epitope. It was used in an  
CC epitope-tagged TATA-box binding protein (TBP) that is expressed by the  
CC transgenic non-human animals of the invention. The animals are used to  
CC produce TBP. TBP is used to isolate and characterise higher-order  
CC transcription complexes (from different tissue and cell types, optionally  
CC at different developmental stages). It is also used to identify new  
CC and/or specific TBP associated factors (TAFs, e.g. transcription factors,  
CC activators or inhibitors) and TAF-interaction factors, and to raise  
CC antibodies against TBP. The TAFs may be useful for regulating gene  
CC expression, e.g. disease-related genes, so are potential pharmaceuticals,  
CC also for identifying human analogues for use in drug screening. The  
CC antibodies are used for affinity purification of TBP and its complexes.  
CC TBP can isolate transcription complexes from a wide variety of different  
CC tissues and cells (contrast known methods that are limited to isolation  
CC from a particular cell type).

XX Sequence 12 AA;

Query Match 81.3%; Score 61; DB 20; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYPYDVPDYA 13  
| | | | |  
Db 2 gpydyvpdy 11

Search completed: April 11, 2002, 10:15:44  
Job time: 94 sec

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	67	89.3	17	4	US-08-789-333F-51	Sequence 51, Appl
2	67	89.3	19	4	US-09-169-0115-52	Sequence 52, Appl
3	65	86.7	16	4	US-09-208-968-15	Sequence 15, Appl
4	61	81.3	11	4	US-09-215-098-4	Sequence 4, Appl
5	61	81.3	14	2	US-08-632-514C-29	Sequence 29, Appl
6	61	81.3	14	3	US-09-188-177-29	Sequence 29, Appl
7	61	81.3	25	1	US-08-634-060-27	Sequence 27, Appl
8	59	78.7	25	2	US-08-700-846-10	Sequence 10, Appl
9	59	78.7	25	2	US-08-672-213-39	Sequence 39, Appl
10	59	78.7	40	4	US-08-672-213-39	Sequence 29, Appl
11	58	77.3	417	1	US-08-199-780-1	Sequence 1, Appl
12	58	77.3	417	2	US-08-316-650-1	Sequence 1, Appl
13	58	77.3	417	5	PCP-US95-02251-1	Sequence 1, Appl
14	56	74.7	32	2	US-09-066-074-7	Sequence 7, Appl
15	56	74.7	32	2	US-08-555-912A-7	Sequence 7, Appl
16	56	74.7	107	1	US-08-625-209A-26	Sequence 26, Appl
17	56	74.7	107	3	US-08-853-733B-26	Sequence 26, Appl
18	56	74.7	115	1	US-08-461-859-34	Sequence 34, Appl
19	56	74.7	219	2	US-08-902-516-2	Sequence 2, Appl
20	55	73.3	9	1	US-08-011-398B-6	Sequence 6, Appl
21	55	73.3	9	1	US-08-090-148-2	Sequence 2, Appl
22	55	73.3	9	1	US-08-370-225-6	Sequence 6, Appl
23	55	73.3	9	1	US-08-167-983-1	Sequence 1, Appl
24	55	73.3	9	1	US-08-634-060-31	Sequence 31, Appl
25	55	73.3	9	1	US-08-464-051-6	Sequence 6, Appl
26	55	73.3	9	1	US-08-461-859-6	Sequence 6, Appl
27	55	73.3	9	1	US-08-470-837-28	Sequence 28, Appl

; SEQ ID NO 52  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-169-015-52

Query Match 89.3%; Score 67; DB 4; Length 19;  
Best Local Similarity 91.7%; Pred. No. 0.00013;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
Db 2 GGGYPYDVPDYA 13

RESULT 3  
US-09-208-966-15  
; Sequence 15, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/208,966  
; CURRENT FILING DATE: 1998-12-10  
; EARLIER APPLICATION NUMBER: 60/082,402  
; EARLIER FILING DATE: 1998-04-20  
; EARLIER APPLICATION NUMBER: 60/069,012  
; EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: human  
US-09-208-966-15

Query Match 86.7%; Score 65; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGYPYDVPDYA 13  
| | | | | | | | | |  
Db 2 SGYPYDVPDYA 12

RESULT 4  
US-09-215-098-4  
; Sequence 4, Application US/09215098  
; Patent No. 6194632  
; GENERAL INFORMATION:  
; APPLICANT: Leiden, Jeffery M  
; TITLE OF INVENTION: DILATED CARDIOMYOPATHY IN TRANSGENIC MICE EXPRESSING A  
; TITLE OF INVENTION: DOMINANT-NEGATIVE CREB TRANSCRIPTION FACTOR IN THE  
; TITLE OF INVENTION: HEART  
; FILE REFERENCE: 9189-4  
; CURRENT APPLICATION NUMBER: US/09/215,098  
; CURRENT FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/068,011  
; PRIOR FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HA peptide tag  
US-09-215-098-4

Query Match 81.3%; Score 61; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00062;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYPYDVPDYA 13  
| | | | | | | | | |  
Db 2 GYPYDVPDYA 11

RESULT 5  
US-08-632-514C-29  
; Sequence 29, Application US/08632514C  
; Patent No. 5834234  
; GENERAL INFORMATION:  
; APPLICANT: GALLO, Gregory J.  
; TITLE OF INVENTION: APOPTOSIS ASSOCIATED PROTEIN BBK  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/632,514C  
; FILING DATE: 29-MAY-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, Henry N.  
; REGISTRATION NUMBER: 32,073  
; REFERENCE/DOCKET NUMBER: 104322.188  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)942-8459  
; TELEFAX: (202)942-8484  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-632-514C-29

Query Match 81.3%; Score 61; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0008;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYPYDVPDYA 13  
| | | | | | | | | |  
Db 2 GYPYDVPDYA 11

RESULT 6  
US-09-188-177-29  
; Sequence 29, Application US/09188177  
; Patent No. 6057132  
; GENERAL INFORMATION:  
; APPLICANT: GALLO, Gregory J.  
; TITLE OF INVENTION: APOPTOSIS ASSOCIATED PROTEIN BBK  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/188,177  
FILING DATE: 2  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, Henry N.  
REGISTRATION NUMBER: 32,073  
REFERENCE/DOCKET NUMBER: 104322.188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)942-8459  
TELEFAX: (202)942-8484  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-188-177-29

Query Match 81.3%; Score 61; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0008;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYPYDVPDYA 13  
| | | | | | | | | |  
DB 2 GYPYDVPDYA 11

RESULT 7  
US-08-634-060-27  
Sequence 27, Application US/08634060  
Patent No. 5712136  
GENERAL INFORMATION:  
APPLICANT: Wickham, Thomas J.  
APPLICANT: Kovesdi, Imre  
APPLICANT: Roelivink, Petrus W.  
TITLE OF INVENTION: ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY  
TITLE OF INVENTION: THE ADENOVIRUS PENTON BASE PROTEIN  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Voit & Mayer, Ltd.  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,060  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/303,162  
FILING DATE: 08-SEP-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kilyk, John Jr.  
REGISTRATION NUMBER: 30763  
REFERENCE/DOCKET NUMBER: 71602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 616-5600

TELEFAX: (312) 616-5700  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-634-060-27

Query Match 78.7%; Score 59; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 0.0031;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
DB 11 GDTYPYDVPDYA 22

RESULT 8  
US-08-700-846-10  
Sequence 10, Application US/08700846  
Patent No. 5962311  
GENERAL INFORMATION:  
APPLICANT: WICKHAM, THOMAS J.  
APPLICANT: ROELVINK, PETRUS W.  
APPLICANT: KOVESDI, IMRE  
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS  
TITLE OF INVENTION: USE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.  
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900  
CITY: CHICAGO  
STATE: IL  
COUNTRY: USA  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,846  
FILING DATE: 21-AUG-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: LARCHER, CAROL  
REGISTRATION NUMBER: 35243  
REFERENCE/DOCKET NUMBER: 74294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 616-5600  
TELEFAX: (312) 616-5700  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-700-846-10

Query Match 78.7%; Score 59; DB 2; Length 25;  
Best Local Similarity 83.3%; Pred. No. 0.0031;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
DB 11 GDTYPYDVPDYA 22

## RESULT 9

US-08-672-213-39  
; Sequence 39, Application US/08672213  
; Patent No. 6306649  
; GENERAL INFORMATION:  
; APPLICANT: GILMAN, Michael Z.  
; APPLICANT: NATESAN, Sridaran  
; TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION  
; TITLE OF INVENTION: FACTORS IN GENE THERAPY  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARIAD Gene Therapeutics, Inc.  
; STREET: 26 Landsdowne Street  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139-4234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,213  
; FILING DATE: 27-JUN-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,553  
; FILING DATE: 27-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/019,614  
; FILING DATE: 29-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BERSTEIN, David L.  
; REGISTRATION NUMBER: 31,235  
; REFERENCE/DOCKET NUMBER: ARIAD 346B  
; TELEPHONE: 617-494-0400  
; TELEFAX: 617-494-0208  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-672-213-39

Query Match 78.7%; Score 59; DB 4; Length 27;  
Best Local Similarity 90.9%; Pred. No. 0.0034; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SGYPYDVPDYA 13  
| | | | | | | | | |  
Db 3 SSYPYDVPDYA 13

## RESULT 10

US-08-672-213-29  
; Sequence 29, Application US/08672213  
; Patent No. 6306649  
; GENERAL INFORMATION:  
; APPLICANT: GILMAN, Michael Z.  
; APPLICANT: NATESAN, Sridaran  
; TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION  
; TITLE OF INVENTION: FACTORS IN GENE THERAPY  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARIAD Gene Therapeutics, Inc.  
; STREET: 26 Landsdowne Street  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA

ZIP: 02139-4234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,213  
; FILING DATE: 27-JUN-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,553  
; FILING DATE: 27-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/019,614  
; FILING DATE: 29-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BERSTEIN, David L.  
; REGISTRATION NUMBER: 31,235  
; REFERENCE/DOCKET NUMBER: ARIAD 346B  
; TELEPHONE: 617-494-0400  
; TELEFAX: 617-494-0208  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-672-213-29

Query Match 78.7%; Score 59; DB 4; Length 40;  
Best Local Similarity 90.9%; Pred. No. 0.0052;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SGYPYDVPDYA 13  
| | | | | | | | | |  
Db 3 SSYPYDVPDYA 13

## RESULT 11

US-08-199-780-1  
; Sequence 1, Application US/08199780  
; Patent No. 5763416  
; GENERAL INFORMATION:  
; APPLICANT: Bonadio, Jeffrey  
; APPLICANT: Goldstein, Steven A.  
; TITLE OF INVENTION: Gene Transfer Into Bone Cells  
; TITLE OF INVENTION: And Tissues  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/199,780  
; FILING DATE: 18-FEB-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UMIC:002  
; TELEPHONE: (512) 320-7200

TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-199-780-1

Query Match 77.3%; Score 58; DB 1; Length 417;  
Best Local Similarity 83.3%; Pred. No. 0.095;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
Db 406 GCRYPDVDPDYA 417

RESULT 12  
US-08-316-650-1  
; Sequence 1, Application US/08316650  
; Patent No. 5942496  
; GENERAL INFORMATION:  
; APPLICANT: Bonadio, Jeffrey  
; APPLICANT: Roessler, Blake J.  
; APPLICANT: Goldstein, Steven A.  
; APPLICANT: Lin, Wushan  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS  
; TITLE OF INVENTION: FOR STIMULATING BONE CELLS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/316,650  
; FILING DATE: 30-SEP-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/199,780  
; FILING DATE: 30-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UMIC:008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-316-650-1

Query Match 77.3%; Score 58; DB 2; Length 417;  
Best Local Similarity 83.3%; Pred. No. 0.095;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
Db 406 GCRYPDVDPDYA 417

RESULT 13  
PCT-US95-02251-1  
; Sequence 1, Application PC/TUS9502251  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING BONE  
; TITLE OF INVENTION: CELLS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
; SOFTWARE: PatentIn Release #1.0, Version  
; SOFTWARE: #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/02251  
; FILING DATE: CONCURRENTLY HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/316,650  
; FILING DATE: 30-SEP-1994  
; CLASSIFICATION:  
; APPLICATION NUMBER: US 08/199,780  
; FILING DATE: 18-FEB-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UMIC009p--  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-02251-1

Query Match 77.3%; Score 58; DB 5; Length 417;  
Best Local Similarity 83.3%; Pred. No. 0.095;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGYPYDVPDYA 13  
| | | | | | | | | |  
Db 406 GCRYPDVDPDYA 417

RESULT 14  
US-09-066-074-7  
; Sequence 7, Application US/09066074  
; Patent No. 5952467  
; GENERAL INFORMATION:  
; APPLICANT: Hunter et al., Tony  
; TITLE OF INVENTION: NIMA INTERACTING PROTEINS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.  
 STREET: 4225 Executive Square, Suite 1400  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/066,074  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/555,912  
 FILING DATE: 13-NOV-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haile, Lisa A.  
 REGISTRATION NUMBER: 38,347  
 REFERENCE/DOCKET NUMBER: 07251/011001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619/678-5070  
 TELEFAX: 619/678-5099  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 32 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 IMMEDIATE SOURCE:  
 CLONE: PGAL-PIN1  
 US-09-066-074-7

Query Match 74.7%; Score 56; DB 2; Length 32;  
 Best Local Similarity 81.8%; Pred. No. 0.012;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SGYPYDVPDYA 13  
 Db 2 ASYPYDVPDYA 12

RESULT 15  
 US-08-555-912A-7  
 Sequence 7, Application US/08555912A  
 Patent No. 5972697  
 GENERAL INFORMATION:  
 APPLICANT: Hunter et al., Tony  
 TITLE OF INVENTION: NIMA INTERACTING PROTEINS  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 4225 Executive Square, Suite 1400  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/555,912A  
 FILING DATE: 13-NOV-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haile, Lisa A.  
 REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07251/011001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619/678-5070  
 TELEFAX: 619/678-5099  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 32 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 IMMEDIATE SOURCE:  
 CLONE: PGAL-PIN1  
 US-08-555-912A-7

Query Match 74.7%; Score 56; DB 2; Length 32;  
 Best Local Similarity 81.8%; Pred. No. 0.012;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SGYPYDVPDYA 13  
 Db 2 ASYPYDVPDYA 12

Search completed: April 11, 2002, 10:14:44  
 Job time: 34 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2002, 10:16:16 ; Search time 27.06 Seconds  
(without alignments)  
36.595 Million cell updates/sec

Title: US-09-284-787-3

Perfect score: 75  
Sequence: 1 SGSPYDVPDYA 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR68:\*

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	56	74.7	347	2 S52188	hemagglutinin - in
2	56	74.7	347	2 S52191	hemagglutinin - in
3	56	74.7	550	1 HMIVS2	hemagglutinin prec
4	56	74.7	550	2 JQ1153	hemagglutinin prec
5	56	74.7	565	1 HMIVET	hemagglutinin prec
6	55	73.3	330	2 JQ2374	hemagglutinin - in
7	55	73.3	330	2 JQ2375	hemagglutinin - in
8	55	73.3	331	2 JQ2377	hemagglutinin - in
9	55	73.3	331	2 JQ2378	hemagglutinin - in
10	55	73.3	347	2 S52173	hemagglutinin - in
11	55	73.3	347	2 S52174	hemagglutinin - in
12	55	73.3	347	2 S52175	hemagglutinin - in
13	55	73.3	347	2 S52176	hemagglutinin - in
14	55	73.3	347	2 S52178	hemagglutinin - in
15	55	73.3	347	2 S52179	hemagglutinin - in
16	55	73.3	347	2 S52180	hemagglutinin - in
17	55	73.3	347	2 S52182	hemagglutinin - in
18	55	73.3	347	2 S52183	hemagglutinin - in
19	55	73.3	347	2 S52185	hemagglutinin - in
20	55	73.3	347	2 S52186	hemagglutinin - in
21	55	73.3	347	2 S52187	hemagglutinin - in
22	55	73.3	347	2 S52189	hemagglutinin - in
23	55	73.3	347	2 S52195	hemagglutinin - in
24	55	73.3	347	2 S52197	hemagglutinin - in
25	55	73.3	347	2 S52199	hemagglutinin - in
26	55	73.3	362	2 S36637	hemagglutinin - in
27	55	73.3	550	1 HMIVS3	hemagglutinin prec
28	55	73.3	550	1 HMIV77	hemagglutinin prec
29	55	73.3	550	1 HMIV80	hemagglutinin prec

ALIGNMENTS

RESULT 1

S52188

hemagglutinin - influenza A virus (isolate A/Guangdong/25/93) (fragment)

C:Species: Influenza A virus

A:Variety: Isolate A/Guangdong/25/93

C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001

C:Accession: S52188

R:Ellis, J.S.

submitted to the EMBL Data Library, October 1994

A:Description: Antigenic and genetic variation in the haemagglutinin of recently circ

A:Reference number: S52173

A:Accession: S52188

A:Molecule type: mRNA

A:Residues: 1-347 <ELL>

A:Cross-references: EMBL:246406; NID:g609049; PIDN:CAA86541.1; PID:g609050

A:Experimental source: Isolate A/Guangdong/25/93

C:Superfamily: Influenza virus hemagglutinin

Query Match 74.7%; Score 56; DB 2; Length 347;  
Best Local Similarity 90.9%; Pred. No. 0.17;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGYPYDVPDYA 13

| | | | | | | | | |

Db 96 SCYPYDVPDYA 106

RESULT 2

S52191

hemagglutinin - influenza A virus (isolate A/Hong Kong/2/94) (fragment)

C:Species: Influenza A virus

A:Variety: Isolate A/Hong Kong/2/94

C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001

C:Accession: S52191

R:Ellis, J.S.

submitted to the EMBL Data Library, October 1994

A:Description: Antigenic and genetic variation in the haemagglutinin of recently circ

A:Reference number: S52173

A:Accession: S52191

A:Molecule type: mRNA

A:Residues: 1-347 <ELL>

A:Cross-references: EMBL:246408; NID:g609055; PIDN:CAA86543.1; PID:g609056

A:Experimental source: Isolate A/Hong Kong/2/94

C:Superfamily: Influenza virus hemagglutinin

Query Match 74.7%; Score 56; DB 2; Length 347;  
Best Local Similarity 90.9%; Pred. No. 0.17;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGYPYDVPDYA 13

Db 96 SCYPYDVPDYA 106  
| | | | | | | | | |

## RESULT 3

HMIVS2  
hemagglutinin precursor - influenza A virus (strain A/swine/126/82) (fragment)  
C:Species: influenza A virus  
C>Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 18-Sep-1998  
C:Accession: A29971  
R:Kida, H.; Shortridge, K.F.; Webster, R.G.

Virolgy 162, 160-166, 1988

A:Title: Origin of the hemagglutinin gene of H3N2 influenza viruses from pigs in China.

A:Reference number: A94370; MUID:88101364

A:Accession: A29971

A:Molecule type: genomic RNA

A:Residues: 1-550 <KID>

A:Cross-references: GB:M19056; NID:g324208

C:Note: the sequence in GenBank entry FLAHAPA, release 106, (PID:g324209) differs from

C:Genetics:

A:Map position: segment 4

C:Superfamily: influenza virus hemagglutinin

C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond

F:1-328/Product: hemagglutinin HA1 #status predicted <HA1>

F:330-550/Product: hemagglutinin HA2 #status predicted <HA2>

F:520-536/Domains: transmembrane #status predicted <TM1>

F:8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:14-466,52-277,64-76,139-473,281-305/Disulfide bonds: #status predicted

F:539,546,549/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 74.7%; Score 56; DB 1; Length 550;

Best Local Similarity 90.9%; Pred. No. 0.27;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGYPYDVPDYA 13

| | | | | | | | | |

Db 96 SCYPYDVPDYA 106

## RESULT 4

JQ1153  
hemagglutinin precursor - influenza A virus (strain A/duck/Hong Kong/7/75) (fragment)  
N:Contains: hemagglutinin HA1; hemagglutinin HA2

C:Species: influenza A virus

C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 20-Jun-2000

C:Accession: JQ1153

R:Yasuda, J.; Shortridge, K.F.; Shimizu, Y.; Kida, H.

J. Gen. Virol. 72, 2007-2010, 1991

A:Title: Molecular evidence for a role of domestic ducks in the introduction of avian H3

A:Reference number: JQ1153; MUID:91341491

A:Accession: JQ1153

A:Molecule type: genomic RNA

A:Residues: 1-550 <YAS>

A:Cross-references: GB:D00929; NID:g221279; PIDN:BAA00769.1; PID:g221280

A:Note: the authors translated the codon GGG for residue 218 as Glu

A:Note: residues 528-532 are not shown in this publication

C:Superfamily: influenza virus hemagglutinin

C:Keywords: glycoprotein; homotrimer

F:1-328/Product: hemagglutinin HA1 #status predicted <HA1>

F:330-545/Product: hemagglutinin HA2 #status predicted <HA2>

F:8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.7%; Score 56; DB 2; Length 550;

Best Local Similarity 90.9%; Pred. No. 0.27;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGYPYDVPDYA 13

| | | | | | | | | |

Db 96 SCYPYDVPDYA 106

## RESULT 5

HMIVET  
hemagglutinin precursor - influenza A virus (strain A/equine/Kentucky/2/86[H3N8])  
N:Contains: hemagglutinin HA1; hemagglutinin HA2

C:Species: influenza A virus

C>Date: 30-Sep-1990 #sequence\_revision 30-Sep-1990 #text\_change 16-Jul-1999

C:Accession: A34065

R:Kawaoka, Y.; Bean, W.J.; Webster, R.G.

Virolgy 169, 283-292, 1989

A:Title: Evolution of the hemagglutinin of equine H3 influenza viruses.

A:Reference number: A34064; MUID:89204899

A:Accession: A34065

A:Molecule type: genomic RNA

A:Residues: 1-565 <RAW>

A:Cross-references: GB:M24727; GB:J04336; NID:g324000; PIDN:AAA43102.1; PID:g324001

C:Genetics:

A:Map position: segment 4

C:Superfamily: influenza virus hemagglutinin

C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond

F:1-16/Domains: signal sequence #status predicted <SIG>

F:17-344/Product: hemagglutinin HA1 #status predicted <HA1>

F:345-565/Product: hemagglutinin HA2 #status predicted <HA2>

F:535-551/Domains: transmembrane #status predicted <TM1>

F:18,23,37,53,68,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status p

F:29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted

F:554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 74.7%; Score 56; DB 1; Length 565;

Best Local Similarity 69.2%; Pred. No. 0.28;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSGYPYDVPDYA 13

| : | | | | | | | |

Db 109 SSNCYPYDIPDYA 121

## RESULT 6

JQ2374  
hemagglutinin - influenza A virus (strain SN1289)

C:Species: influenza A virus

C>Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999

C:Accession: JQ2374

R:Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.

J. Gen. Virol. 74, 2513-2518, 1993

A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtain

A:Reference number: JQ2369; MUID:94065682

A:Accession: JQ2374

A:Molecule type: mRNA

A:Residues: 1-330 <ROC>

A:Cross-references: GB:L20115

A:Experimental source: subtype H3N2

C:Superfamily: influenza virus hemagglutinin

Query Match 73.3%; Score 55; DB 2; Length 330;

Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13

| | | | | | | |

Db 98 YPYDVPDYA 106

## RESULT 7

JQ2375  
hemagglutinin - influenza A virus (strain SN1389 and IN0190)

C:Species: influenza A virus

C>Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999

C:Accession: JQ2375; JQ2376

R:Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.

J. Gen. Virol. 74, 2513-2518, 1993

A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtain

A:Reference number: JQ23769; MUID:94065682

A:Accession: JQ2375

A:Molecule type: mRNA

A:Residues: 1-330 <ROC>

A:Cross-references: GB:L20119

A:Experimental source: subtype H3N2

C:Superfamily: Influenza virus haemagglutinin

Query Match 73.3%; Score 55; DB 2; Length 330;

Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13

|||||

Db 98 YPYDVPDYA 106

RESULT 8

JQ2377

hemagglutinin - Influenza A virus (strain SD0191)

C:Species: Influenza A virus

C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999

C:Accession: JQ2377

R:Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.

J. Gen. Virol. 74, 2513-2518, 1993

A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained

A:Reference number: JQ23769; MUID:94065682

A:Accession: JQ2377

A:Molecule type: mRNA

A:Residues: 1-331 <ROC>

A:Cross-references: GB:L20105

A:Experimental source: subtype H3N2

C:Superfamily: Influenza virus haemagglutinin

Query Match 73.3%; Score 55; DB 2; Length 331;

Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13

|||||

Db 98 YPYDVPDYA 106

RESULT 9

JQ2378

hemagglutinin - Influenza A virus (strain HI0191)

C:Species: Influenza A virus

C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999

C:Accession: JQ2378

R:Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.

J. Gen. Virol. 74, 2513-2518, 1993

A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained

A:Reference number: JQ23769; MUID:94065682

A:Accession: JQ2378

A:Molecule type: mRNA

A:Residues: 1-331 <ROC>

A:Cross-references: GB:L20102

A:Experimental source: subtype H3N2

C:Superfamily: Influenza virus haemagglutinin

Query Match 73.3%; Score 55; DB 2; Length 331;

Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13

|||||

Db 98 YPYDVPDYA 106

RESULT 10

JQ2379

hemagglutinin - Influenza A virus (isolate A/Beijing/353/89) (fragment)

C:Species: Influenza A virus

A:Variety: isolate A/Beijing/353/89

C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 20-Sep-1999

C:Accession: S52174

S52173

hemagglutinin - Influenza A virus (fragment)

C:Species: Influenza A virus

C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001

C:Accession: S52173; S52190; S52192; S52177; S52181; S52194; S52196; S52184; S52193

R:Ellis, J.S.

submitted to the EMBL Data Library, October 1994

A:Description: Antigenic and genetic variation in the haemagglutinin of recently circ

A:Reference number: S52173

A:Accession: S52173

A:Molecule type: mRNA

A:Residues: 1-347 <ELL>

A:Cross-references: EMBL:Z46392; NID:g609020; PIDN:CAA86527.1; PID:g609021

A:Experimental source: isolate A/Beijing/32/92

A:Accession: S52190

A:Molecule type: mRNA

A:Residues: 1-347 <EL2>

A:Cross-references: EMBL:Z46410; NID:g609053; PIDN:CAA86545.1; PID:g609054

A:Experimental source: isolate A/Hong Kong/23/92

A:Accession: S52192

A:Molecule type: mRNA

A:Residues: 1-347 <EL3>

A:Cross-references: EMBL:Z46409; NID:g609057; PIDN:CAA86544.1; PID:g609058

A:Experimental source: isolate A/Hong Kong/34/90

A:Accession: S52177

A:Molecule type: mRNA

A:Residues: 1-134, 'K', 136-156, 'L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227

A:Cross-references: EMBL:Z46395; NID:g609027; PIDN:CAA86530.1; PID:g1228087

A:Experimental source: isolate A/England/269/93

A:Accession: S52181

A:Molecule type: mRNA

A:Residues: 1-134, 'K', 136-156, 'L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227

A:Cross-references: EMBL:Z46399; NID:g609035; PIDN:CAA86534.1; PID:g609036

A:Experimental source: isolate A/England/328/93

A:Accession: S52194

A:Molecule type: mRNA

A:Residues: 1-134, 'K', 136-156, 'L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227

A:Cross-references: EMBL:Z46414; NID:g609061; PIDN:CAA86549.1; PID:g609062

A:Experimental source: isolate A/Scotland/160/93

A:Accession: S52196

A:Molecule type: mRNA

A:Residues: 1-134, 'K', 136-156, 'L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227

A:Cross-references: EMBL:Z46415; NID:g609065; PIDN:CAA86550.1; PID:g609066

A:Experimental source: isolate A/Scotland/174/93

A:Accession: S52184

A:Molecule type: mRNA

A:Residues: 1-74, 'N', 76-120, 'T', 122-156, 'L', 158-173, 'F', 175-188, 'S', 190-200, 'K', 202-2

A:Cross-references: EMBL:Z46402; NID:g609041; PIDN:CAA86537.1; PID:g609042

A:Experimental source: isolate A/England/471/93

A:Accession: S52193

A:Molecule type: mRNA

A:Residues: 1-74, 'N', 76-120, 'T', 122-156, 'L', 158-173, 'F', 175-188, 'S', 190-200, 'K', 202-2

A:Cross-references: EMBL:Z46413; NID:g609059; PIDN:CAA86548.1; PID:g609060

A:Experimental source: isolate A/Scotland/142/93

C:Superfamily: Influenza virus haemagglutinin

Query Match

Best Local Similarity 100.0%; Pred. No. 0.24;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13

|||||

Db 98 YPYDVPDYA 106

RESULT 11

S52174

R;Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circula  
A:Reference number: S52173  
A:Accession: S52174  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:Z46391; NID:g609022; PIDN:CAA86536.1; PID:g609023  
A:Experimental source: isolate A/Beijing/353/89  
C:Superfamily: influenza virus hemagglutinin

Query Match 73.3%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13  
|||||

Db 98 YPYDVPDYA 106

RESULT 12  
S52175  
hemagglutinin - influenza A virus (isolate A/England/1/93) (fragment)  
C:Species: influenza A virus  
A:Variety: isolate A/England/1/93  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52175  
R;Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circula  
A:Reference number: S52173  
A:Accession: S52175  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:Z46393; NID:g609024; PIDN:CAA86528.1; PID:g940547  
A:Experimental source: isolate A/England/1/93  
C:Superfamily: influenza virus hemagglutinin

Query Match 73.3%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13  
|||||

Db 98 YPYDVPDYA 106

RESULT 13  
S52176  
hemagglutinin - influenza A virus (isolate A/England/247/93) (fragment)  
C:Species: influenza A virus  
A:Variety: isolate A/England/247/93  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52176  
R;Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circula  
A:Reference number: S52173  
A:Accession: S52176  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:Z46394; NID:g609025; PIDN:CAA86529.1; PID:g609026  
A:Experimental source: isolate A/England/247/93  
C:Superfamily: influenza virus hemagglutinin

Query Match 73.3%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13

Db 98 YPYDVPDYA 106  
|||||

RESULT 14  
S52178  
hemagglutinin - influenza A virus (isolate A/England/284/93) (fragment)  
C:Species: influenza A virus  
A:Variety: isolate A/England/284/93  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52178  
R;Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circ  
A:Reference number: S52173  
A:Accession: S52178  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:Z46396; NID:g609029; PIDN:CAA86531.1; PID:g609030  
A:Experimental source: isolate A/England/284/93  
C:Superfamily: influenza virus hemagglutinin

Query Match 73.3%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13  
|||||

Db 98 YPYDVPDYA 106

RESULT 15  
S52179  
hemagglutinin - influenza A virus (isolate A/England/286/93) (fragment)  
C:Species: influenza A virus  
A:Variety: isolate A/England/286/93  
C:Date: 07-May-1995 #sequence\_revision 23-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: S52179  
R;Ellis, J.S.  
submitted to the EMBL Data Library, October 1994  
A:Description: Antigenic and genetic variation in the haemagglutinin of recently circ  
A:Reference number: S52173  
A:Accession: S52179  
A:Molecule type: mRNA  
A:Residues: 1-347 <ELL>  
A:Cross-references: EMBL:Z46397; NID:g609031; PIDN:CAA86532.1; PID:g609032  
A:Experimental source: isolate A/England/286/93  
C:Superfamily: influenza virus hemagglutinin

Query Match 73.3%; Score 55; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13  
|||||

Db 98 YPYDVPDYA 106

Search completed: April 11, 2002, 10:16:16  
Job time: 126 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2002, 10:22:00 ; Search time 18.1 Seconds  
(without alignments)  
26.334 Million cell updates/sec

Title: US-09-284-787-3  
Perfect score: 75  
Sequence: 1 SSGYPPYDVPDYA 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	74.7	550	HEMA_IADHK	P43257 Influenza a
2	56	74.7	550	HEMA_IADH3	P11134 Influenza a
3	56	74.7	565	HEMA_IADH6	P16999 Influenza a
4	55	73.3	249	HEMA_IADH1	P03438 Influenza a
5	55	73.3	328	HEMA_IADH6	P04664 Influenza a
6	55	73.3	328	HEMA_IADH7	P04663 Influenza a
7	55	73.3	550	HEMA_IADH1	P03441 Influenza a
8	55	73.3	550	HEMA_IADH2	P12582 Influenza a
9	55	73.3	550	HEMA_IADH3	P12583 Influenza a
10	55	73.3	550	HEMA_IADH4	P12584 Influenza a
11	55	73.3	550	HEMA_IADH5	P12585 Influenza a
12	55	73.3	550	HEMA_IADH6	P12587 Influenza a
13	55	73.3	550	HEMA_IADH7	P12588 Influenza a
14	55	73.3	550	HEMA_IADH8	P43258 Influenza a
15	55	73.3	550	HEMA_IADH9	P43259 Influenza a
16	55	73.3	550	HEMA_IADH10	P43260 Influenza a
17	55	73.3	550	HEMA_IADH11	P12589 Influenza a
18	55	73.3	550	HEMA_IADH12	P11133 Influenza a
19	55	73.3	565	HEMA_IADH13	P16994 Influenza a
20	55	73.3	565	HEMA_IADH14	P15658 Influenza a
21	55	73.3	566	HEMA_IADH15	P03437 Influenza a
22	55	73.3	566	HEMA_IADH16	P26135 Influenza a
23	55	73.3	566	HEMA_IADH17	P03440 Influenza a
24	55	73.3	566	HEMA_IADH18	P03449 Influenza a
25	55	73.3	566	HEMA_IADH19	P03449 Influenza a
26	55	73.3	566	HEMA_IADH20	P03439 Influenza a
27	55	73.3	566	HEMA_IADH21	P03436 Influenza a
28	55	73.3	566	HEMA_IADH22	P19106 Influenza a
29	55	73.3	566	HEMA_IADH23	P26139 Influenza a
30	55	73.3	567	HEMA_IADH24	P03435 Influenza a
31	54	72.0	565	HEMA_IADH25	P16995 Influenza a
32	54	72.0	565	HEMA_IADH26	P16996 Influenza a
33	54	72.0	565	HEMA_IADH27	P16997 Influenza a

34	54	72.0	565	1	HEMA_IADH28	P16998 Influenza a
35	54	72.0	565	1	HEMA_IADH29	P16999 Influenza a
36	54	72.0	565	1	HEMA_IADH30	Q08011 Influenza a
37	54	72.0	565	1	HEMA_IADH31	P17001 Influenza a
38	54	72.0	565	1	HEMA_IADH32	P17002 Influenza a
39	54	72.0	566	1	HEMA_IADH33	P03442 Influenza a
40	51	68.0	566	1	HEMA_IADH34	P26134 Influenza a
41	51	68.0	566	1	HEMA_IADH35	P26141 Influenza a
42	50	66.7	565	1	HEMA_IADH36	P17000 Influenza a
43	47	62.7	550	1	HEMA_IADH37	P12586 Influenza a
44	47	62.7	563	1	HEMA_IADH38	P26137 Influenza a
45	47	62.7	564	1	HEMA_IADH39	P16964 Influenza a

#### ALIGNMENTS

RESULT 1  
HEMA\_IADHK STANDARD; PRT; 550 AA.  
AC P43257;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;  
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).  
GN HA.  
OS Influenza A virus (strain A/Duck/Hong Kong/7/75).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses;  
OC Influenza A virus.  
OX NCBI\_TaxID=11364;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91341491; PubMed=1875195;  
RA Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;  
RT "Molecular evidence for a role of domestic ducks in the introduction  
RT of avian H3 influenza viruses to pigs in southern China, where the  
RT A/Hong Kong/68 (H3N2) strain emerged.";  
RL J. Gen. Virol. 72:2007-2010(1991).  
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
CC CELL RECEPTORS AND FOR INITIATING INFECTION.  
CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
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CC -----  
CC EMBL; D00929; BAA00769.1; -;  
CC HSSP; P03437; SHMG.  
CC InterPro; IPR001364; Hemagglutn.  
CC Pfam; PF00509; Hemagglutinin; 1.  
CC ProDom; PD000225; Hemagglutn; 1.  
KW Envelope protein; Hemagglutinin; Glycoprotein.  
FT NON\_TER 1  
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.  
FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.  
FT CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 550 AA; 61549 MW; 864639B829FE1BA9 CRC64;

Query Match 74.7%; Score 56; DB 1; Length 550;





20-AUG-2001 (Rel. 40, Last annotation update)  
 HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAL CHAIN]  
 GN HA.  
 OS Influenza A virus (strain X-31).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses;  
 OC Influenza A virus.  
 OX NCBI\_TaxID=11489;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81030852; PubMed=7421990;  
 RA Gething M.J., Bye J., Stehel J.J., Waterfield M.;  
 RT "Cloning and DNA sequence of double-stranded copies of haemagglutinin  
 genes from H2 and H3 strains elucidates antigenic shift and drift in  
 human influenza virus.";  
 RL Nature 287:301-306(1990).  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
 CC CELL RECEPTORS AND FOR INITIATING INFECTION.  
 CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
 CC (HAL AND HA2) LINKED BY A DISULFIDE BOND.  
 CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
 DR PIR: A04051; HMIVH.  
 DR PIR: A93233; A93233.  
 DR HSP: P03437; SHMG.  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 KW Envelope protein; Hemagglutinin; Glycoprotein; Signal.  
 FT SIGNAL 1 16 HEMAGGLUTININ HAL CHAIN.  
 FT CARBOHYD 17 >249  
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 249 249  
 FT SEQUENCE 249 AA; 27373 MW; 9537AA970BB79183 CRC64;  
 Query Match 73.3%; Score 55; DB 1; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 0.055;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 YPYDVPDYA 13  
 DB 114 YPYDVPDYA 122  
 RESULT 5  
 HEMA\_IAENG STANDARD; PRT; 328 AA.  
 ID HEMA\_IAENG  
 AC P04664;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HAL CHAIN] (FRAGMENT).  
 GN HA.  
 OS Influenza A virus (strain A/England/878/69).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses;  
 OC Influenza A virus.  
 OX NCBI\_TaxID=11377;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81194918; PubMed=6164798;  
 RA Sleight M.J., Both G.W., Underwood P.A., Bender V.J.;  
 RT "Antigenic drift in the hemagglutinin of the Hong Kong influenza  
 RT subtype: correlation of amino acid changes with alterations in viral  
 RT antigenicity.";  
 RL J. Virol. 37:845-853(1981).  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
 CC CELL RECEPTORS AND FOR INITIATING INFECTION.

-1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
 (HAL AND HA2) LINKED BY A DISULFIDE BOND.  
 -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
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 EMBL: K03335; AAA43184.1; -  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 KW Envelope protein; Hemagglutinin; Glycoprotein.  
 FT NON\_TER 1 1  
 FT CHAIN 1 328 HEMAGGLUTININ HAL CHAIN.  
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 328 328  
 FT SEQUENCE 328 AA; 36072 MW; 9C3A86B3A8D856FE CRC64;  
 Query Match 73.3%; Score 55; DB 1; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 0.072;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 YPYDVPDYA 13  
 DB 98 YPYDVPDYA 106  
 RESULT 6  
 HEMA\_IAQU7 STANDARD; PRT; 328 AA.  
 ID HEMA\_IAQU7  
 AC P04663;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HAL CHAIN] (FRAGMENT).  
 GN HA.  
 OS Influenza A virus (strain A/Qu/7/70).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses;  
 OC Influenza A virus.  
 OX NCBI\_TaxID=11456;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81194918; PubMed=6164798;  
 RA Sleight M.J., Both G.W., Underwood P.A., Bender V.J.;  
 RT "Antigenic drift in the hemagglutinin of the Hong Kong influenza  
 RT subtype: correlation of amino acid changes with alterations in viral  
 RT antigenicity.";  
 RL J. Virol. 37:845-853(1981).  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
 CC CELL RECEPTORS AND FOR INITIATING INFECTION.  
 CC -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
 CC (HAL AND HA2) LINKED BY A DISULFIDE BOND.  
 CC -1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
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 or send an email to license@isb-sib.ch).

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CC EMBL; K03338; AAA43195.1; -.
DR InterPro: IPR001364; Hemagglutn.
DR Pfam: PF00509; Hemagglutinin; 1.
DR ProDom: PD000225; Hemagglutn; 1.
KW Envelope protein; Hemagglutinin; Glycoprotein.
FT NON_TER 1 1
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 328
SQ SEQUENCE 328 AA; 36059 MW; E30A962FD6D805B CRC64;

Query Match 73.3%; Score 55; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YPYDVPDYA 13
Db 98 YPYDVPDYA 106

RESULT 7
HEMA_IABAN
ID HEMA_IABAN STANDARD; PRT; 550 AA.
AC P03441; Q83961; Q83962;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Bangkok/1/79).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11325;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82033259; PubMed=6169840;
RA Both G.W., Sleight M.J.;
RT "Conservation and variation in the hemagglutinins of Hong Kong
RT subtype influenza viruses during antigenic drift.";
RL J. Virol. 39:663-672(1981).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC or send an email to license@isb-sib.ch).
```

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FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 550 AA; 61699 MW; FBD2EC200689CB5 CRC64;

Query Match 73.3%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YPYDVPDYA 13
Db 98 YPYDVPDYA 106

RESULT 8
HEMA_IADH1
ID HEMA_IADH1 STANDARD; PRT; 550 AA.
AC P12582; Q84021; Q84022;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hokkaido/5/77).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11357;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87265458; PubMed=2440178;
RA Kida H., Kawaoaka Y., Naevé C.W., Webster R.G.;
RT "Antigenic and genetic conservation of H3 influenza virus in wild
RT ducks.";
RL Virology 159:109-119(1987).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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Query Match 73.3%; Score 55; DB 1; Length 550;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13  
|||||

DB 98 YPYDVPDYA 106

## RESULT 9

HEMA\_IADH2 STANDARD; PRT; 550 AA.  
AC P12583; Q84011;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;  
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).  
GN HA.  
OS Influenza A virus (strain A/Duck/Hokkaido/8/80).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses;  
OC Influenza A virus.  
OX NCBI\_TaxID=11358;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87265458; PubMed=2440178;  
RA Kida H., Kawakawa Y., Naeye C.W., Webster R.G.;  
RT "Antigenic and genetic conservation of H3 influenza virus in wild  
RT ducks.";  
RL Virology 159:109-119(1987).  
CC -I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
CC CELL RECEPTORS AND FOR INITIATING INFECTION.  
CC -I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
CC -I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: M16738; AAA43144.1; -  
CC PIR: B27813; HMIV80.  
CC InterPro: IPR001364; Hemagglutn.  
CC Pfam: PF00509; Hemagglutinin; 1.  
CC ProDom: PD000225; Hemagglutn; 1.  
KW Envelope protein; Hemagglutinin; Glycoprotein.  
FT NON\_TER 1 1 HEMAGGLUTININ HA1 CHAIN.  
FT CHAIN 1 328 HEMAGGLUTININ HA2 CHAIN.  
FT CHAIN 330 550 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CONFLICT 137 137 K -> N (IN PIR DATA BANK).  
SQ SEQUENCE 550 AA; 61659 MW; A107023ACC9CC353 CRC64;

Query Match 73.3%; Score 55; DB 1; Length 550;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13  
|||||

DB 98 YPYDVPDYA 106

## RESULT 10

HEMA\_IADH3 STANDARD; PRT; 550 AA.  
AC P12584; Q84012; Q89793;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;  
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).  
GN HA.  
OS Influenza A virus (strain A/Duck/Hokkaido/33/80).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses;  
OC Influenza A virus.  
OX NCBI\_TaxID=11359;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87265458; PubMed=2440178;  
RA Kida H., Kawakawa Y., Naeye C.W., Webster R.G.;  
RT "Antigenic and genetic conservation of H3 influenza virus in wild  
RT ducks.";  
RL Virology 159:109-119(1987).  
CC -I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
CC CELL RECEPTORS AND FOR INITIATING INFECTION.  
CC -I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
CC -I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: M16739; AAA43145.1; -  
CC PIR: C27813; HMIV33.  
CC InterPro: IPR001364; Hemagglutn.  
CC Pfam: PF00509; Hemagglutinin; 1.  
CC ProDom: PD000225; Hemagglutn; 1.  
KW Envelope protein; Hemagglutinin; Glycoprotein.  
FT NON\_TER 1 1 HEMAGGLUTININ HA1 CHAIN.  
FT CHAIN 1 328 HEMAGGLUTININ HA2 CHAIN.  
FT CHAIN 330 550 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 550 AA; 61577 MW; 6C30BF67CFDCB7DE CRC64;

Query Match 73.3%; Score 55; DB 1; Length 550;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13  
|||||

DB 98 YPYDVPDYA 106

## RESULT 11

HEMA\_IADH4 STANDARD; PRT; 550 AA.  
AC P12585; Q84013; Q84014;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;  
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).  
GN HA.

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OS Influenza A virus (strain A/Duck/Hokkaido/7/82).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87265458; PubMed=2440178;
RA Kida H., Kawaoka Y., Naeye C.W., Webster R.G.;
RT "Antigenic and genetic conservation of H3 influenza virus in wild
RT ducks.";
RL Virology 159:109-119(1987).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M16740; AAA43146.1; -.
CC PIR: D27813; HMIIV89.
CC InterPro: IPR001364; Hemagglutn.
CC Pfam: PF00509; Hemagglutinin; 1.
CC ProDom: PD000225; Hemagglutn; 1.
CC Envelope protein; Hemagglutinin; Glycoprotein.
CC NON_TER 1 1
CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 550 AA; 61664 MW; A16B2CF8CBBBD9D0 CRC64;
FT FT
FT NON_TER 1 1
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 550 AA; 61664 MW; A16B2CF8CBBBD9D0 CRC64;
SQ

Query Match 73.3%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13
Db 98 YPYDVPDYA 106
|||||

RESULT 12
HEMA_IADH6 STANDARD; PRT; 550 AA.
AC P12587; Q84017;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hokkaido/9/85).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11362;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87265458; PubMed=2440178;
RA Kida H., Kawaoka Y., Naeye C.W., Webster R.G.;
RT "Antigenic and genetic conservation of H3 influenza virus in wild
RT ducks.";
RL Virology 159:109-119(1987).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC -----
CC EMBL: M16740; AAA43146.1; -.
CC PIR: D27813; HMIIV89.
CC InterPro: IPR001364; Hemagglutn.
CC Pfam: PF00509; Hemagglutinin; 1.
CC ProDom: PD000225; Hemagglutn; 1.
CC Envelope protein; Hemagglutinin; Glycoprotein.
CC NON_TER 1 1
CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 550 AA; 61664 MW; A16B2CF8CBBBD9D0 CRC64;
FT FT
FT NON_TER 1 1
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 550 AA; 61664 MW; A16B2CF8CBBBD9D0 CRC64;
SQ

```

```

RT ducks.";
RL Virology 159:109-119(1987).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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CC -----
CC EMBL: M16742; AAA43148.1; -.
CC PIR: F27813; HMIIV98.
CC InterPro: IPR001364; Hemagglutn.
CC Pfam: PF00509; Hemagglutinin; 1.
CC ProDom: PD000225; Hemagglutn; 1.
CC Envelope protein; Hemagglutinin; Glycoprotein.
CC NON_TER 1 1
CC CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
CC CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
CC CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CONFLICT 8 8 Y -> N (IN PIR DATA BANK).
CC SEQUENCE 550 AA; 61711 MW; 67BCD85F44736CFE CRC64;
FT FT
FT NON_TER 1 1
FT CHAIN 1 328 HEMAGGLUTININ HA1 CHAIN.
FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 8 8 Y -> N (IN PIR DATA BANK).
FT SEQUENCE 550 AA; 61711 MW; 67BCD85F44736CFE CRC64;
SQ

Query Match 73.3%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13
Db 98 YPYDVPDYA 106
|||||

RESULT 13
HEMA_IADH7 STANDARD; PRT; 550 AA.
AC P12588; Q84018; Q89470;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
GN HA.
OS Influenza A virus (strain A/Duck/Hokkaido/10/85).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses;
OC Influenza A virus.
OX NCBI_TaxID=11363;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87265458; PubMed=2440178;
RA Kida H., Kawaoka Y., Naeye C.W., Webster R.G.;
RT "Antigenic and genetic conservation of H3 influenza virus in wild
RT ducks.";
RL Virology 159:109-119(1987).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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 CC -----

DR EMBL: M16743; AAA43149.1; -  
 DR PIR: G27813; HMIV15.  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 KW Envelope protein; Hemagglutinin; Glycoprotein.  
 FT NON\_TER 1 1  
 FT CHAIN 1 328 HEMAGGLUTININ HAI CHAIN.  
 FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.  
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 550 AA; 61761 MW; 6EF81793281D53EB CRC64;

Query Match 73.3%; Score 55; DB 1; Length 550;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 YPYDVPDYA 13  
 |||||  
 DB 98 YPYDVPDYA 106

RESULT 14

ID HEMA\_IADHL STANDARD; PRT; 550 AA.  
 AC P43238;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;  
 DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).  
 GN HA.  
 OS Influenza A virus (strain A/Duck/Hong Kong/64/76).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses;  
 OC Influenza A virus.  
 OX NCBI\_TaxID=45412;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91341491; PubMed=1875195;  
 RA Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;  
 RT "Molecular evidence for a role of domestic ducks in the introduction  
 RT of avian H3 influenza viruses to pigs in southern China, where the  
 RT A/Hong Kong/68 (H3N2) strain emerged.";  
 RL J. Gen. Virol. 72:2007-2010(1991).  
 CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
 CC CELL RECEPTORS AND FOR INITIATING INFECTION.  
 CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
 CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
 CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
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 CC -----  
 DR EMBL: D00931; BAA00771.1; -  
 DR HSSP: P03437; 2HMG.  
 DR InterPro: IPR001364; Hemagglutn.

DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 KW Envelope protein; Hemagglutinin; Glycoprotein.  
 FT NON\_TER 1 1  
 FT CHAIN 1 328 HEMAGGLUTININ HAI CHAIN.  
 FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.  
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 550 AA; 61718 MW; A351C56789E4BE9A CRC64;

Query Match 73.3%; Score 55; DB 1; Length 550;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 YPYDVPDYA 13  
 |||||  
 DB 98 YPYDVPDYA 106

RESULT 15

ID HEMA\_IADHM STANDARD; PRT; 550 AA.  
 AC P43259;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;  
 DE HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).  
 GN HA.  
 OS Influenza A virus (strain A/Duck/Hong Kong/231/77).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses;  
 OC Influenza A virus.  
 OX NCBI\_TaxID=45411;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91341491; PubMed=1875195;  
 RA Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;  
 RT "Molecular evidence for a role of domestic ducks in the introduction  
 RT of avian H3 influenza viruses to pigs in southern China, where the  
 RT A/Hong Kong/68 (H3N2) strain emerged.";  
 RL J. Gen. Virol. 72:2007-2010(1991).  
 CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO  
 CC CELL RECEPTORS AND FOR INITIATING INFECTION.  
 CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS  
 CC (HA1 AND HA2) LINKED BY A DISULFIDE BOND.  
 CC -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.  
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 CC -----  
 DR EMBL: D00932; BAA00772.1; -  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 KW Envelope protein; Hemagglutinin; Glycoprotein.  
 FT NON\_TER 1 1  
 FT CHAIN 1 328 HEMAGGLUTININ HAI CHAIN.  
 FT CHAIN 330 550 HEMAGGLUTININ HA2 CHAIN.  
 FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 483 483 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 550 AA; 61762 MW; 6FEF8B49488C191A CRC64;

Query Match 73.3%; Score 55; DB 1; Length 550;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13  
 |||||  
 Db 98 YPYDVPDYA 106

Search completed: April 11, 2002, 10:22:01  
 Job time: 431 sec

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OM protein - protein search, using sw model

Run on: April 11, 2002, 10:22:57 ; Search time 50.04 Seconds  
(without alignments)  
38.000 Million cell updates/sec

Title: US-09-284-787-3  
Perfect score: 75  
Sequence: 1 SGSCYPDVPDYA 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: SPTRMBL17.\*
- 2: sp-archaea.\*
- 3: sp-bacteria.\*
- 4: sp-fungi.\*
- 5: sp-human.\*
- 6: sp\_invertebrate.\*
- 7: sp\_mhc.\*
- 8: sp-organelle.\*
- 9: sp-phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	74.7	329	12 O40850	O40850 influenza a
2	56	74.7	329	12 O40764	O40764 influenza a
3	56	74.7	329	12 O40820	O40820 influenza a
4	56	74.7	344	12 Q98083	Q98083 influenza a
5	56	74.7	347	12 Q82787	Q82787 influenza a
6	56	74.7	347	12 Q82790	Q82790 influenza a
7	56	74.7	565	12 Q9WA90	Q9WA90 influenza a
8	55	73.3	236	12 Q9W821	Q9W821 influenza a
9	55	73.3	236	12 Q9W829	Q9W829 influenza a
10	55	73.3	236	12 Q9W8J7	Q9W8J7 influenza a
11	55	73.3	286	12 Q9W126	Q9W126 influenza a
12	55	73.3	286	12 Q9W125	Q9W125 influenza a
13	55	73.3	286	12 Q9W124	Q9W124 influenza a
14	55	73.3	325	12 O40774	O40774 influenza a
15	55	73.3	325	12 Q9DL45	Q9DL45 influenza a
16	55	73.3	326	12 O40779	O40779 influenza a
17	55	73.3	326	12 O40780	O40780 influenza a
18	55	73.3	327	12 O92324	O92324 influenza a
19	55	73.3	327	12 O92325	O92325 influenza a

20	55	73.3	327	12 O92327	O92327 influenza a
21	55	73.3	327	12 Q9YT90	Q9YT90 influenza a
22	55	73.3	327	12 Q9YT89	Q9YT89 influenza a
23	55	73.3	327	12 Q9YT88	Q9YT88 influenza a
24	55	73.3	327	12 Q9YT87	Q9YT87 influenza a
25	55	73.3	327	12 Q9YT86	Q9YT86 influenza a
26	55	73.3	327	12 Q9YR09	Q9YR09 influenza a
27	55	73.3	327	12 Q9YR08	Q9YR08 influenza a
28	55	73.3	327	12 Q9YR07	Q9YR07 influenza a
29	55	73.3	327	12 Q9YR06	Q9YR06 influenza a
30	55	73.3	327	12 Q9YR05	Q9YR05 influenza a
31	55	73.3	327	12 Q9YR04	Q9YR04 influenza a
32	55	73.3	327	12 Q9YR03	Q9YR03 influenza a
33	55	73.3	327	12 Q9YJ57	Q9YJ57 influenza a
34	55	73.3	327	12 Q9YIN9	Q9YIN9 influenza a
35	55	73.3	327	12 Q9Q884	Q9Q884 influenza a
36	55	73.3	328	12 O40855	O40855 influenza a
37	55	73.3	328	12 O40867	O40867 influenza a
38	55	73.3	328	12 Q82567	Q82567 influenza a
39	55	73.3	328	12 Q82568	Q82568 influenza a
40	55	73.3	328	12 Q82569	Q82569 influenza a
41	55	73.3	328	12 Q82578	Q82578 influenza a
42	55	73.3	328	12 Q82579	Q82579 influenza a
43	55	73.3	328	12 Q82580	Q82580 influenza a
44	55	73.3	328	12 Q82581	Q82581 influenza a
45	55	73.3	328	12 Q82575	Q82575 influenza a

ALIGNMENTS

RESULT 1  
O40850 PRELIMINARY; PRT; 329 AA.  
ID O40850;  
AC O40850;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE HEMAGGLUTININ (FRAGMENT).  
OS HA.  
GN Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group; Influenza A viruses.  
OX NCBI\_taxid=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/WUZHOU/1/94(H3N2);  
RA Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;  
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).  
DR EMBL; AF008858; AAB69800.1; ...  
DR InterPro; IPR001364; Hemagglutn.  
DR Pfam; PF00509; Hemagglutinin; 1.  
DR ProDom; PD000225; Hemagglutn; 1.  
FT NON\_TER 1  
FT NON\_TER 329  
SQ SEQUENCE 329 AA; 36562 MW; 9DDICA9187D537DF CRC64;

Query Match 74.7%; Score 56; DB 12; Length 329;  
Best Local Similarity 90.9%; Pred. No. 0.29;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGYPDVPDYA 13  
| | | | | | | | | |  
Db 96 SCYPDVPDYA 106

RESULT 2  
O40764 PRELIMINARY; PRT; 329 AA.  
ID O40764;  
AC O40764;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE HAEMAGGLUTININ GENE (FRAGMENT).  
 GN HA.  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses.  
 OX NCBI\_TaxID=11320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/HONG\_KONG/1/94 (H3N2);  
 RA Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF008772; AAB63709.1; -;  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 DR NON\_TER 1  
 FT NON\_TER 329 329  
 FT NON\_TER 329 329  
 SQ SEQUENCE 329 AA; 36630 MW; D1DF31668818FA8D CRC64;

Query Match 74.7%; Score 56; DB 12; Length 329;  
 Best Local Similarity 90.9%; Pred. No. 0.29;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 SGYPYDVPDYA 13  
 Db 96 SCYPYDVPDYA 106  
 I | | | | | | | | | |

RESULT 3  
 O40820 PRELIMINARY; PRT; 329 AA.  
 AC O40820;  
 DT 01-JAN-1998 (Tremblrel. 05, Created)  
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE HAEMAGGLUTININ GENE (FRAGMENT).  
 GN HA.  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses.  
 OX NCBI\_TaxID=11320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/GUANGDONG/25/93 (H3N2);  
 RA Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF008828; AAB63765.1; -;  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 DR NON\_TER 1  
 FT NON\_TER 329 329  
 FT NON\_TER 329 329  
 SQ SEQUENCE 329 AA; 36566 MW; 4DD909217213F423 CRC64;

Query Match 74.7%; Score 56; DB 12; Length 329;  
 Best Local Similarity 90.9%; Pred. No. 0.29;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 SGYPYDVPDYA 13  
 Db 96 SCYPYDVPDYA 106  
 I | | | | | | | | | |

RESULT 4  
 Q98083 PRELIMINARY; PRT; 344 AA.  
 AC Q98083;  
 DT 01-FEB-1997 (Tremblrel. 02, Created)  
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE HAEMAGGLUTININ (FRAGMENT).  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses.  
 OX NCBI\_TaxID=11320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/GUANGDONG/28/94 (H3N2);  
 RA MEDLINE=96370797; PubMed=8774693;  
 RA Lindstrom S., Sugita S., Endo A., Ishida M., Huang P., Xi S.H.,  
 RA Nerome K.;  
 RT "Evolutionary characterization of recent human H3N2 influenza A  
 RT isolates from Japan and China: novel changes in the receptor binding  
 RT domain";  
 RL Arch. Virol. 141:1349-1355(1996).  
 DR EMBL: U48442; AAB09416.1; -;  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 DR CHAIN 17 >344  
 FT NON\_TER 344 344  
 FT NON\_TER 344 344  
 SQ SEQUENCE 344 AA; 38139 MW; C5A8CC7DBB0ACBAE CRC64;

Query Match 74.7%; Score 56; DB 12; Length 344;  
 Best Local Similarity 90.9%; Pred. No. 0.31;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 SGYPYDVPDYA 13  
 Db 112 SCYPYDVPDYA 122  
 I | | | | | | | | | |

RESULT 5  
 Q82787 PRELIMINARY; PRT; 347 AA.  
 AC Q82787;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE HAEMAGGLUTININ (FRAGMENT).  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses.  
 OX NCBI\_TaxID=11320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/GUANGDONG/25/93;  
 RX MEDLINE=96105347; PubMed=7503689;  
 RA Ellis J.S., Chakraverty P., Clewley J.P.;  
 RT "Genetic and antigenic variation in the haemagglutinin of recently  
 RT circulating human influenza A (H3N2) viruses in the United Kingdom.";  
 RL Arch. Virol. 140:1889-1904(1995).  
 DR EMBL: Z46406; CAA86541.1; -;  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
 DR NON\_TER 1  
 FT NON\_TER 347 347  
 FT NON\_TER 347 347  
 SQ SEQUENCE 347 AA; 38368 MW; 441AF1B0BE1F594B CRC64;

Query Match 74.7%; Score 56; DB 12; Length 347;  
 Best Local Similarity 90.9%; Pred. No. 0.31;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 SGYPYDVPDYA 13  
 Db 96 SCYPYDVPDYA 106  
 I | | | | | | | | | |

RESULT 6  
 Q82790



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ID Q82790 PRELIMINARY; PRT; 347 AA.
AC Q82790;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE HAEMAGGLUTININ (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses.
OX NCBI_TaxID=11320;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=A/HONG KONG/2/94;
RX MEDLINE=96105347; PubMed=7503689;
RA Ellis J.S., Chakraverty P., Clewley J.P.;
RT "Genetic and antigenic variation in the haemagglutinin of recently
RT circulating human influenza A (H3N2) viruses in the United Kingdom.";
RL Arch. Virol. 140:1889-1904(1995).
DR EMBL: Z46408; CAA86543.1; -;
DR InterPro: IPR001364; Hemagglutn.
DR Pfam: PF00509; Hemagglutinin; 1.
DR ProDom: PD000225; Hemagglutn; 1.
FT NON_TER 1
FT 347
SQ SEQUENCE 347 AA; 38379 MW; C29A4400E80F8635 CRC64;

Query Match 74.7%; Score 56; DB 12; Length 347;
Best Local Similarity 90.9%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGYPYDPDYA 13
DB 96 SCYPYDPDYA 106

RESULT 7
Q9WA90 PRELIMINARY; PRT; 565 AA.
ID Q9WA90;
AC Q9WA90;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE INFLUENZA A/EQUINE/KENTUCKY/2/86 (H3N8) HAEMAGGLUTININ (HA) RNA (SEG.
DE 4), COMPLETE CDS.
OS Influenza A virus (strain A/Equine/Kentucky/2/86).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=11403;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=89204899; PubMed=2705299;
RA Kawaka Y., Bean W.J., Webster R.G.;
RT "Evolution of the haemagglutinin of equine H3 influenza viruses.";
RL Virology 169:283-292(1989).
DR EMBL: M24727; AAA43102.1; -;
DR InterPro: IPR001364; Hemagglutn.
DR Pfam: PF00509; Hemagglutinin; 1.
DR PRINTS; PR00329; HAEMAGGLUTN12.
DR ProDom: PD000225; Hemagglutn; 1.
FT CHAIN 1 344 POTENTIAL.
FT CHAIN 345 565 POTENTIAL.
SQ SEQUENCE 565 AA; 63592 MW; EB9FEFF/CBB861DB CRC64;

Query Match 74.7%; Score 56; DB 12; Length 565;
Best Local Similarity 69.2%; Pred. No. 0.55;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGCGPYDPDYA 13
DB 109 SSNCYPYDPDYA 121

```

```

RESULT 8
Q9W8Z1 PRELIMINARY; PRT; 236 AA.
ID Q9W8Z1;
AC Q9W8Z1;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE HAEMAGGLUTININ (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses.
OX NCBI_TaxID=11320;
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RN SEQUENCE FROM N.A.
RP STRAIN=TOKYO157, TOKYO1511;
RA Mori S., Sekine H.;
RT "HA1 domain of Influenza A (H3N2) virus.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB013807; BAA77285.1; -;
DR EMBL: AB013806; BAA77284.1; -;
DR InterPro: IPR001364; Hemagglutn.
DR Pfam: PF00509; Hemagglutinin; 1.
DR PRINTS; PR00329; HAEMAGGLUTN12.
DR ProDom: PD000225; Hemagglutn; 1.
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FT 236
SQ SEQUENCE 236 AA; 26477 MW; 4566C8E7210FB558 CRC64;

Query Match 73.3%; Score 55; DB 12; Length 236;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YPYDVPDYA 13
DB 11 YPYDVPDYA 19

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ID Q9W8T9;
AC Q9W8T9;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE HAEMAGGLUTININ (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses.
OX NCBI_TaxID=11320;
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RN SEQUENCE FROM N.A.
RP STRAIN=TOKYO157, TOKYO1566, TOKYO1567, TOKYO1568, TOKYO1569;
RA Mori S., Sekine H.;
RT "HA1 domain of Influenza A (H3N2) virus.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB013813; BAA77291.1; -;
DR EMBL: AB013809; BAA77287.1; -;
DR EMBL: AB013810; BAA77288.1; -;
DR EMBL: AB013811; BAA77289.1; -;
DR EMBL: AB013812; BAA77290.1; -;
DR InterPro: IPR001364; Hemagglutn.
DR Pfam: PF00509; Hemagglutinin; 1.
DR PRINTS; PR00329; HAEMAGGLUTN12.
DR ProDom: PD000225; Hemagglutn; 1.
FT NON_TER 1
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Query Match 73.3%; Score 55; DB 12; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.29;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 11 YPYDVPDYA 19
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AC Q9W8J7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HEMAGGLUTININ (FRAGMENT).
GN HA.
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-72, 70, AND 71;
RA Nagashima M., Mori S., Sekine H.;
RT "Influenza A virus gene for hemagglutinin.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-TOKYO1539;
RA Mori S., Sekine H.;
RT "HA1 domain of Influenza A (H3N2) virus.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB014062; BAA77294.1; -
DR EMBL; AB013808; BAA77286.1; -
DR EMBL; AB014060; BAA77292.1; -
DR EMBL; AB014061; BAA77293.1; -
DR InterPro; IPR001364; Hemagglutn.
DR Pfam; PF00509; Hemagglutinin; 1.
DR PRINTS; PR00329; HEMAGGLUTN12.
DR ProDom; PD000225; Hemagglutn; 1.
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Db 11 YPYDVPDYA 19
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AC Q9WI26;
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DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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GN HA.
OS Influenza A virus (A/Taiwan/2034/96(H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=95241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/TAIWAN/2034/96;
RA Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
RT "Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in Taiwan.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AFI39936; AAD34853.1; -
DR InterPro; IPR001364; Hemagglutn.
DR Pfam; PF00509; Hemagglutinin; 1.
DR PRINTS; PR00329; HEMAGGLUTN12.
DR ProDom; PD000225; Hemagglutn; 1.
FT NON_TER 1
FT NON_TER 236
SQ SEQUENCE 236 AA; 32059 MW; CB51B092AAD0D7D8 CRC64;

Query Match 73.3%; Score 55; DB 12; Length 286;
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DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE H3 HEMAGGLUTININ (FRAGMENT).
GN HA.
OS Influenza A virus (A/Taiwan/2191/96(H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=95236;
RN [1]
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Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
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DR Pfam; PF00509; Hemagglutinin; 1.
DR PRINTS; PR00329; HEMAGGLUTN12.
DR ProDom; PD000225; Hemagglutn; 1.
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FT NON_TER 286
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Db 57 YPYDVPDYA 65
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DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE H3 HEMAGGLUTININ (FRAGMENT).
GN HA.
OS Influenza A virus (A/Taiwan/2192/96(H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=95240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/TAIWAN/2192/96;
RA Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
RT "Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in Taiwan.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AFI39936; AAD34853.1; -
DR InterPro; IPR001364; Hemagglutn.
DR Pfam; PF00509; Hemagglutinin; 1.
DR PRINTS; PR00329; HEMAGGLUTN12.
DR ProDom; PD000225; Hemagglutn; 1.
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Query Match 73.3%; Score 55; DB 12; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 YPYDVPDYA 13
Db 57 YPYDVPDYA 65
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AC Q9WI24;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE H3 HEMAGGLUTININ (FRAGMENT).
GN HA.
OS Influenza A virus (A/Taiwan/2191/96(H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group; Influenza A viruses; Influenza A virus.
OX NCBI_TaxID=95236;
RN [1]
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RP SEQUENCE FROM N.A.  
 RC STRAIN=A/TAIWAN/2191/96;  
 RA Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;  
 RT "Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in  
 RT Taiwan";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF139932; AAD34849.1; -;  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR PRINTS; PR00329; HEMAGGLUTN12.  
 DR ProDom: PD000225; Hemagglutn; 1.  
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QY 5 YPYDVPDYA 13  
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 Db 57 YPYDVPDYA 65

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 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEMAGGLUTININ GENE (FRAGMENT).  
 GN HA.  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses.  
 OX NCBI\_TaxID=11320;  
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 RN SEQUENCE FROM N.A.  
 RC STRAIN=A/ILLINOIS/5/95(H3N2);  
 RA Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF008782; AAB63719.1; -;  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR ProDom: PD000225; Hemagglutn; 1.  
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 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEMAGGLUTININ (FRAGMENT).  
 OS Influenza A virus (A/Finland/583/98(H3N2)).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza virus A and B group; Influenza A viruses;  
 OX NCBI\_TaxID=147149;

RN SEQUENCE FROM N.A.  
 RC STRAIN=A/FINLAND/583/98;  
 RA Pyhala R., Haanpaa M., Kleemola M., Tervahauta R., Visakorpi R.,  
 RA Kinnunen L.;  
 RT "Acceptable protective efficacy of influenza vaccination in young  
 RT military conscripts in circumstances of incomplete antigenic and  
 RT genetic match";  
 RL Vaccine 0:0-0(2001).  
 DR EMBL: AF311689; AAG47810.1; -;  
 DR InterPro: IPR001364; Hemagglutn.  
 DR Pfam: PF00509; Hemagglutinin; 1.  
 DR PRINTS; PR00329; HEMAGGLUTN12.  
 DR ProDom: PD000225; Hemagglutn; 1.  
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 FT NON\_TER 1 325  
 SQ SEQUENCE 325 AA; 36029 MW; 5BECB8CC3E83B1C2 CRC64;

Query Match 73.3%; Score 55; DB 12; Length 325;  
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QY 5 YPYDVPDYA 13  
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 Db 98 YPYDVPDYA 106

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